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Mon Nov
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- nucleic search, using sw model OM nucleic

October 30, 2004, 12:45:36; Search time 6341 Seconds (without alignments) 11388.010 Million cell updates/sec Run on:

US-09-604-231-1 1527

score: Perfect

1 ctcatggcatctgcgccgtt......gttgaaaccttgagtgttcg 1527 Scoring table: Sequence:

IDENTITY NUC Gapox 1.0

4526729 seqs, 23644849745 residues Searched:

Total number of hits satisfying chosen parameters:

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length: 0 length: 2000000000 DB seq DB seq Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

gb_sy:* gb_un:* gb_vi:* gb htg: *
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gb ov: *
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gb pt: *
gb pt: * gb_sts:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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ID	AX069134	AX469820	AP005282	BX927155	AX127152	AX122988	BD165105	BD093238	AX069136	AL935252	PDCRAFOPER	PPSURFOP	AF401046	LLZ97015	AE004395	STRSCRA	AE015011	AY177419	AE017206
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AX926712 Sequence AE006222 Pasteurel M76768 Vibrito algi X69800 S.xylosus s Z54245 B.subtilis D8367 Bacillus su D86417 Bacillus su	acillus tion (26 Staphyl	AP004830 Straphyloc AP003137 Staphyloc AP003365 Staphyloc AF269422 Staphyloc AR485378 Sequence		AX621496 Sequence AL646084 Ralstonia ABO16921 Chromobac AR396402 Sequence AE016833 Enterococ
AX926712 AB006222 VIBSCRAK SXSCRA BSTREAPR D83967 D86417	BSUB0005 BX571856_25 AC090968_ BX571857_24	AP004830 AP003137 AF269422 AR485378	AX144742 AB016750 AP001514 AX131006 AX432414	AX621496 AL646084 AE016921 AR396402 AE016833
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ALIGNMENTS

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Patent: WO 0102583-A 11-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE) Corynebacterium glutamicum Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium 101 1507 note="unnamed protein product; RXS00315" linear 1. .1527 /organism="Corynebacterium glutamicum" DNA /mol_type="unassigned DNA" /db_xref="taxon:1718" 101. .1507 /transl_table=11 |protein_id="CAC27276.1" |db_xref="GI:12579017" AX069134 1527 bp Sequence 1 from Patent W00102583 Location/Qualifiers AGANLLNVAKKEAVPATP" AX069134 AX069134.1 GI:12579016 /codon_start=1 /transl_table= DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM source AUTHORS TITLE JOURNAL RESULT 1 AX069134 REFERENCE FEATURES CDS LOCUS

Gaps ö Length 1527; Indels DB 6; ; 0 Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches

ORIGIN

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8 8 8 8 8	8 64 B	රු අ රු අ	Qy Db	RESULT 3 APO05282/c LOCUS	ACCESSION VERSION	SOURCE ORGA	REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE	JOURNAL	COMMENT FEATURES sou		6 C	
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CTCATGGCATCTGCGCTTCTTGCCAGTTGTTGGTTGGTTTCACGGCAACCAAG 60 Db 1 CTCATGGCATCTGCGGTTCTTGCCAGTTTCACGGCAACCAAG 60 QY 61 CGTTTCGGCGCAATTCCTGGGCGCTATTGGTATTGGTATTCCCGAG 120 Db 61 CGTTTCGGCGCAATGAGTTCCTGGGCGCGCATTGGTATTGGTATTCCCGAG 120 Db 61 CGTTTCGGCGCAATGAGTTCCTGGGCGCCACTATGGCTATTGGCGATGGTGTTCCCGAG 120 QY 121 CTTGGTGAACGGCTACGACGCCCCCCCCCACTATGGCTGCCACAATGGCTATTGTGGTC 180 Db 121 CTTGGTGAACGGCTACGACGCCCACCACGAGGGCGACAATGTGGTC 180 Db 121 CTTGGTGAACGGCTACGACGACCACCACGAGGAGGAAATGCCAATGTGGTC 180	181 CCTGTTTGGTTTAGATGTTGCCCAAGCCGGGTTACCAGGGCACCGTGCTTCTTGCTTG	ATCGC ATCGC CTTTA	421 TGATTTCGGTCCAGTCGGCGTCTGCTCTTCGGTCTACTCACCAATCGTCAT	Qy 481 CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGTGTTTAACCAGGTGGATC 540 Db 481 CACTGGTCTGCACCAGTCCTTCCCGGCCAATTGAGCTGGAGCTGTTTAACCAGGTGGATC 540	Qy 541 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCCGCATGTTTGGCAGT 600 DD 541 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCCGCCATGTTTGGCAGT 600	Oy 601 GTTCTTCCTGGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTCTCCGC 660	661 TGTTCTTGGTATTACGGAGCCTGCGATCTTCGGTGTGAACCTTCGCCTGCGCTGGCGTT 720 [Oy 721 CTTCATCGGTATCGGTACCCCAGCTATCGGTGGCGCTTTGATTGCACTCTTTAATATCAA 780 Db 721 CTTCATCGGTATCGGTACCGCAGCTATCGGTGGCGCTTTGATTGCACTCTTTAATATCAA 780	Qy 781 GCCAGTIGCGTIGGGCGCTGCAGATITCTIGGGCGTGTTGTTTCTATTGATGCTCCAGATAT 840 Db 781 GGCAGTIGCGTIGGGCGCTGCAGATITCTTGGGTGTTGTTTCTATTGATGCTCCAGATAT 840	Qy 841 GGTCATGTTCTTGGTGTGTGCAGTTGTTACCTTCTCGTCGCATTCGGCAGCGATTGC 900	9) TTATGGCCTTTACTTGGTTCGCCGCAACGCAGCATTGATCCAGATGCAACGGCTGCTCC 960	OY 961 AGTGCCTGCAGGAACGACCAAAGCCGAAGAAGCACCCGCAGAATTTCAAACGATTC 1020 	OY 1021 CACCATCATCCAGGCACCTTTGACCGGTGAAGCTATTGCACTGAGCAGCGTCAGCGGATGC 1080

gene

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TMQPGRWNDMDEGSKGTLVALKDALWALRAQIAGAPEGEAANDPERFAERQNLSNHLM
EIHDANVRILEVFAEEDPSKQYDVVWHNHDDRRGDSLNVAPLSVAGLLHEKLFAENTV
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BETLDEI YELLTAAGGRTLGLESSKRAABQATKARAILLEPPDVLCQBDNTAALVKK
FSDSENTCLFGTLITHQGVDVPGRSLSLULIDRI PFPREDDPLLQARKRAADAGGROG
FSDSENTCLFGTLITHQGVDVPGRSLSLULIDRI PFPREDDPLLQARKRAADAGGROG
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(protein id="BAB99912.1"
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complement (5587. .6312)
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2866. .4608
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CGAAATTGAAGCGGGAGCCAACCTGCTCAACGTCGCAAAGAAGAAGCGGTGCCAGCAAC 146579
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Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

(Dases 1 to 349136)
Ralinowski,J., Bathe,B., Bartels,D., Bischoff,N., Bott,M.,
Burkovski,A., Dusch,M., Huthmacher,K., Kramer,R., Inke,B.,
Goesmann,A., Hartmann,M., Huthmacher,K., Kramer,R., Inke,B.,
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and Tauch,A.
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                                                                                           147238 GGTCATGTTCTTGGTGTGTGCAGTTGTTACTTCTTCATCGCATTCGCGCGCAGCGATTGC
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Corynebacterium glutamicum ATCC
complete genome; segment 8/10.
BX927155 BX927147
BX927155.1 GI:41326514
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                                                               / LTAIN 1 ALL 1 ONE "MAADS DESCRIBAYLKEHVAPVKAINWNS I PDSKDLEVWDRLIGN
FWLPEKVPVSNDI KSWGTLNEVEKAATWRVFTGLTLLDTI QGTVGA I SILLPDADSLHE
EAVLTNI AFWESVHAKGSNI FWTLASTAEINDAFRWEEBENENLORKKI I LEYYEGD
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LNNLGYEGLFPADETKVSPNI LSALSPNADENHDFFSGSGSSYVI GKRARNTEDDDWDF
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                                                                                                                                                                                                                                                                                             Length 320550
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Pred. No. 0;
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/gene="cgl2526"
11555. .12043
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TITLE

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SNTFIVYSIVSSTSIAALFNAGVGPCLLMIIACVIVGTWIARKENYKKRQIHFTFKQS
LVVLWRALPSLLMIVIVVGGILLGWFTPTSAALAVYCUVLGFIYRTIKVGDLADIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSTAWIANNDIGKIYSLAHDIANNIYKLIGEWETGYPEGGGEPDAEGIVAATNGDIYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPVGDWVELANTDNNNSIDISGWSLVDDKEDLENALVLPEGTEIESGGYFVIYTDSAD
YVPTNNTFGGQEYFGLGKDDTVTLRNAEGEVVATYSWKDLGEHAENTYGRIPDMTGDF
ANTGVPTPGAKNVAAEGSGEEEGVVANAQLPPHNVEITPIHLGGDFTGEDMSGVDFDA
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ELLGGGLKIGFTELESTNIAPIVDAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'translation="MPPSFFPRRKKSEPDLLALPAQIRDVHADVLDIFMAESLVIINI
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/transl_table=11
/product= "PUTATIVE C4-DICARBOXYLATE TRANSPORT SYSTEM
(PERMEASE LARGE PROTEIN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ģ
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'product="putative secreted protein"
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db xref="GI:41326518"
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complement(7072. .8385)
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4836. .6431
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/transl_table=11
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6556. .6942
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3674. .4672
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/transl_table=
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/transl_table=
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ESRFDDLRLRVPLLIHGHLHSQFPWTGPGQVDVGVEAMGLKPAPRELVQLKLWESLSE
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TEGIAGRLIDWMAIIATLFGTAATLGLSAIQVGGCVQIISGASEITNNILLAIIALIT
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SMACKSLSWCEETIEFQAGWTAFYWAWWIAWTPFVGMFIARISRGRTLREFALITWAI
PSFILLLAFTIFGGTAITWNRRNVDGPDGSSSKEQVLFDMFSNLPLYSITPFILIFVL
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NLTILIAIPPALVLIVMAIAPIKDLSTDPAAIRQRYAKAAISNAVVRGLEEHGDDFEL
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complete Corynebacterium glutamicum ATCC 13032 genome sequence its impact on the production of L-aspartate-derived amino acids
                                                                                                                                                                                                                                                                                                                                       Submitted (21-3NN-2004) Joern Kalinowski, Institut fuer Genomforschung, Universitate Bielefeld, Universitaetsstrasse 25, 38615 Bielefeld, Germany Germ

    .349136
/organism="Corynebacterium glutamicum ATCC 13032"

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/product="hypothetical protein predicted by
Glimmer/Critica"
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codon_start=1

cansi_tansle=1:

[product="ECTOINE BETAINE TRANSPORTER"
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complement (67. .729)
/locus tag="cg2562"
complement (67. .729)
                                                                                                              J. Biotechnol. 104 (1-3), 5-25 (2003) 22830012
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complement(3014. .3295)
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830. .2722
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'trans1_table=
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/gene="lcoP"
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481 CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGGTGGATC 540 339656 CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGGTGGATC 339597 541 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGAGTGTTTGGCAGT 600	339476	781 GGCAGTTGCGTTGGGCTGCAGGTTTCTTGGGTGTTTCTATTGATGCTCCAGATAT 840 339356 GGCAGTTGCGTTGCAGGTTTCTTGGGTGTTTCTATTGATGCTCCAGATAT 339297 841 GGTCATGTTCTTGGTGCAGGTTTCTTGGGTGTTTCTTCATCGCGCGCAGCGATTGT 339297 842 GGTCATGTTCTTGGTGTGCAGTTTGTTACCTTCTTCATCGCATTCGGCGCAGCGATTGC 339237 339296 GGTCATGTTTACTTGGTGTGCCGCACCGATCGCATTCGCCATCGGCGCAGCGATTGC 339237 901 TTATGGCCTTTACTTGGTTCGCCGCAACGCAGCATTGATCCAGATGCACCGCTGCTCC 960 339236 TTATGGCCTTTACTTGGTTCGCCGCAGCAGTTGATCCAGATGCAACCGCTGCTCC 339177 961 AGTGCCTTACTTGGTTCGCCGCAAGCCGAATTGATCCAGATCGCAACCGCTCCTCC 339177	1021 CACCATCATCCAGGAACCAAAGCCCACAAATTTTCAAACGATCC 1880 139116 CACCATCATCCAGGAACCAAAGCCAATTTTCAACCACCACCACCACCATCC 1081 CACCATCATCCAGGACCTTTGACCGGTCAACCATTTGACCACTCAACCACCACCACCACCACCACCACCACCACCAC
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/locus_tag="cg256 complement(8387. /gene="dctx" /locus_tag="cg256 /codon_start=1 /transl_table=11 /producT="PUTAITY (PERMEASS SMALL) /protein_id="CAF" /db_xref="G1:4133" /translation="MM AFLEGREGHIAUDFIAN ITALPITIGREGHIAUDFIAN ITALPITIGREGHIAUDFIAN GSAIDSASSABGRN"	gene complement(89089657) /gene="dctp" /locus tag="g2570" /gene="dctp" /locus tag="g2570"	/transl_table=11 /product="puparive c4-Dicarboxxlate-BinDing ProTein" /product="puparive c4-Dicarboxxlate-BinDing ProTein" /protein_id="CaF21065.1" /db_xref="d1:4132652" /translation="MMGSVERRYIRSFDMFTTPEVGVIGSIEHQMSVIRDQDLMEPL FQSIEBDDISYNGGFTQGTRUNTYTDAPPRYRRADLAGRKIRVOBSAMITMIELMGG SATPLIYGEVTAMQSGVLDGABRNEISYVRQNHFEVARXNSNTNHLVGLDXMVMRHD LLDAMSEPDRELFLEEMDAAMTEHTDLMNTETDAVIERGARGAEFVEVDAQAFTDAL APIKDEFLYEBFQRELYEAVRADTSGGAAS" Complement (972211569) /gene="lepa" /locus_tag="cg2571" complement (972211569) /qene="lepa" /locus_tag="cg2571"	//codon_arart=1 //codon_ar

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/db_xref="taxon:1718"
/note="Seq 1 to long (3.309.400) split in 11, seq 7068
2.700.001 3.049.980"
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                           Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A. Novel polymucleotides
Patent: EP 1108790-A 7068 20-JUN-2001;
KXOWA HAKKO KOGYO CO., LID. (JP)
Location/Qualifiers
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Best Local Similarity 99.2%;
Matches 1526; Conservative
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Sequence 7068 from
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Corynebacterineae; Corynebacteriaceae; Corynebacterium. AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., TITLE Novel polynucleotides JOURNAL Patent: EP 1108790-A 2904 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP) FEATURES Source / Organism="Corynebacterium glutamicum" / Mol_type="unassigned DNA" // Mol_type="unassigned DNA" // Mb_xref="taxon:1718"	Ouery Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1503; Conservative 0; Mismatches 0; Indels 1; Gaps 1; Oy 1 CTCATGGCATCTGCGCTTCTTGCCAGTGTTGGTTGGTTGACCGCAACCAAG 60 Db 481 CTCATGGCATCTGCGGTTCTTGCCAGTGTTGGTTTGATTTCACCGCAACCAAG 540	CGAG CGAG CGAG	181 660 241	Db 720 GGTTTCTTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCCAAGGGCACTGC 779 Qy 301 AGACTTCCTGATCGAGGGCTCCACGAGATTCCTGCAAGGGCACTGC 779 Qy 301 AGACTTCCTGATCACCAGGTGCTGACGTGCTGCTGCTGCTACATTCATCGC 360	QY 361 CANTGGCCCAGCAATGCGCTGGCTGGCTGGCACACGGTCTACAGGGACTTTA 420 Db 840 CANTGGCCCAGCAATGCGCTGGGCGATGTGCTGGCACACGGTCTACAGGGACTTTA 899 QY 421 TGAATTCGGTGGTCCAGTCGGCGTCTGCTCTTCGGTCTACTCACCCAATCGTCAT 480 Db 900 TGATTTCGGTGGTCCAGTCGGCGTTTCGGTCTTCGGTCTACTCACCAATCGTCAT 959	481 CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGCAGCTGTTTAACCAGGGTGGATC 540	09 601 GTTCTTCCTGGCGAAGGTGAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTCTCCGC 60

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Izui,M., Sugimoto,M., Nakamatsu,T. and Kurahashi,O.
Dana encoding sucrose PTS enzyme II Patent: WO 0102584-A 11.JAN-2001;
AJINOMOTO CO INC,MASAKO IZUI,MASAKAZU SUGIMOTO,TSUYOSHI NAKAMATSU,
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PC G01N33/566,

PC G12N1/21, C12R1:13), (C12N1/21, C12R1:01), (C12P13/08, C12R1:15),

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    CTACATTGGTATCGGTACCGCAGCTATCGGTGGCGCTTTGATTGCACTCTTTGATATCAA 5037
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Patent: WO 0102583-A 311-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
                                                                                                               GGTCATGTTCTTGGTTTGCGCGGTAGTTACCTTTGTCATCGCATTCGCGCAGCGATTGC
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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30-JUN-2000 WO 2000JP004348
02-JUL-1999 JP 99P 189512
MASAKO IZUI,MASAKAZU SUGIMOTO,TSUYOSHI NAKAMATSU,OSAMU
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0; Mismatches
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WO 0102584-A/1
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Best Local Similarity 95.7%;
Matches 1462; Conservative (
   KURAHASHI
OSAMU KURA
OS Brevi
PN WO 011-JA
PF 30-JU
PR MASAK
KURAHASHI
PC C12N1
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Kuipers,O.P., Leer,R., Tarchini,R., Peters,S.A., Sandbrink,H.M.,
Fiers,M.W.E.J., Stiekema,W., Lankhorst,R.M.K., Bron,P.A.,
Hoffer,S.M., Groct,M.N.N., Kerkhoven,R., de Vries,M., Ursing,B.,
Vos,W.M. and Siezen,R.J.
Complete genome sequence of Lactobacillus plantarum WCFS1
Proc. Natl. Acad. Sci. U.S.A. 100 (4), 1990-1995 (2003)
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Lactobacillus plantarum WCFS1
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Kleerebezem,M. and Slezen,R.J.
Direct Submission
Submitted (14-OTT-2002) Wageningen Centre for
Box 557, 6700 AN Wageningen, The Netherlands
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Pred. No. 4.8e-288;
0; Mismatches 1;
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EVMGQLAPSPKPVVQRYKGLGEMDAEQLMETTMDPDKRRLLRVRDEDAADADGVFSML
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LESRAESEHQAANGSGNNNYNNGNSNYNNNNNGYSNQGQNAAPQQSSANNNNFFGN
GNTGNASSAAPSSSANNNNQADFFANNGDQIDISDDDLFF"
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GIKTANVTEKNGHLAGLITVDGQEDIMVMTNQGVMIRFNIATVSQTGRATLGVRLMRL
GDDGQVATMAKVDFEPEVDETVATDATTEAPVDDQTVNADATTTEPTTDSNDSNE"
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protein id="CAD62710.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                    MGDQVKPRREFIEDNAKFVQDLDV"
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/EC_number="5.99.1.3"
/codon_start=1
/transl_table=11
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/gene="rpsf"
/locus_tag="lp_0009"
9860. .10159
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6676. .9237
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10196._.10798
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'transl table=
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'gene="ssb"
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/gene="gyrA"
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Leenhouts, K.J., Bolhnis, A.A., Kok, J.J. and Venema, G.G.
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
Unpublished (1994)
On May 25, 1994 this sequence version replaced gi:475106.
Original source text: Pediococcus pentosaceus (strain PPE1.0) DNA;
Insertion sequence IS30 homolog (transposable element Insertion
sequence IS30 homolog, kingdom Prokaryotae) DNA; Pediococcus
pentosaceus (strain PPE1.0) DNA; Insertion sequence IS3 homolog
(transposable element Insertion sequence IS3 homolog
(transposable element Insertion sequence IS3 homolog
Prokaryotae) DNA; and Pediococcus pentosaceus (strain PPE1.0) DNA.
Location/Qualifiers
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ESPATAQVRXTEQFNLAYGSTLGRNYSTGCTIMD.CHYLMLSRSYLYTLFKTHANTSP
OKLLIKURLEDAKQRLSTSNNSVQSIANWYGYKDSFTFSKAFKRXSGASPSYYKKSIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           permease; rafP
                                                                                                                                                                                                                                                                                                                                                                                                                                           agaR gene, agaS gene, agl gene, alpha-galactosidase, permease, rafi alpha-gluosidase, fructokinase, insertion element, permease, rafi gene, rafR gene, raffinose operon; regulatory protein, scrA gene, scrB gene; scrR gene, scrR gene, sucrase, sucrose-6-phosphate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pediococcus pentosaceus
Pediococcus pentosaceus
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                             linear
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Pediococcus pentosaceus raffinose operon genes.
L32093
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/organisma="Pediococcus pe
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/db xref="taxon:1255"
/Apt.-510
/note="DR2; putative"
/rpt type=direct
488. .561
/note="IR1; putative"
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/protein_id="AAA25562.1"
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/gene="rafR"
3909. .5918
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2724. .2760
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/transl_table=3
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                                                                         AGCGATTGCTTATGGC
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16532 CACGACTGGTTGGATTGGCATGGGCATCTTTGGCCTTCTACTACTCGGCCATTGTCATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- AACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166232 ATTTCCATTTGTCTTTGCAGCGATTGCCTCAGGAATTGCTTCAGCTTTCTTAGGACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 GGGTGGATCCTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166352 Triradcrafrircriraccacrafadadccafafadadcafadaccrafacrrcricadcod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAATATCAAGGCAGTTGCGTTGGGCGCTGCAGGTTTCTTGGGTGTTTCTTGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCAGATATGGTCATGTTCTTGGTGTGTGCAGTTGTTACCTTCTTCATCGCATTCGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCTCCGCTGTTCTTGGTATTACGGAGCCTGCGATCTTCGGTGTGAACCTTCGCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712 CTGGCCGTTCTTCATCGGTATCGGTACCGCAGCTATCGGTGGCGCTTTGATTGCACTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCGGCGCCAATGAGTTCCTGGGCGCCGCGTATTGGTATGGCGATGGTGTTCCCGAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGGCAGTGTTCTTCCTGGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGTGCTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trodereceaeccorarcies de recentado en esta en 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGAACGGCTACGACGTGGCCGCCACCATGGCTGCGGGCGAAATGCCAATGTGGTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGTGCTGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166772 CTTTGGTTTACACGTTGCACAAGCAGGCTATCAAGGCCAAGTGCTCCCTGTTTTGGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCAAGGGCACTGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCTGATCACTCCAGTGCTGACGTTGCTGCTCACCGGGATTCCTTACATTCATCGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 TGGCCCAGCAATGCGCTGGGTGGGCGATGTGCTGGCACACACGGTCTACAGGGACTTTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                            Length 343050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                Score 308.4; DB 1;
Pred. No. 1.4e-71;
0; Mismatches 351;
                                                                                                                                                                        /locus_tag="lp_0011"
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/transl_table=11
/product="ribosomal_protein_S18"
/protein_id="CAD62711.1"
                                                                             locus_tag="lp_0011"
       .11073
                                                                                                         .11073
                                                                                                                                                                                                                                                                                                                                                                                   20.2%;
                                                                                                                                        gene="rpsR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                         .0837
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652
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Best Local S
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/note="putative"
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/transl_table=11
/product="alpha-galactosidase"
/protein_id="AAAA25566.1"
/db_xref="cd:475111"
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YFEPMRSGSRARANDQIPERFPYSKHTEVTTLVIHLTDAVTKLQMDLANTIFENQPLILES
                                                                                                                                                    TDVNEAAYGESMIGIAKDVPNSIYMTIGTGVGAGYISQNHIFNGRTHTELGHMELNRL.
PGDDFKSNCPYHDICLEGLAAGPAVGKRTGKAGKDIPVDDPVWPIITDYIAQACVNLT
VAFAPDKIILNGGVMNQRQLFPMIREKFAAYLNGYEEVPPLDDYIVPAGLGNNSGIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILRHHGTTNILQVTALSSAQIDI.PTDQYTALTILSGTRAHEANPS FNRIHPGI.COVRSI.
RGTSGPQHQPPMALAEPNTTELAGTVI GCALAWSGNFDSTVEVDQYQHSRLTIGLEPD
TFWQLKPNSSFQTPEAVLYWTNITGRNGMSQVFHDPSSYQLMFSCTNINFSTLT
GVARSSKVQHLI BHAHGLQMLVLDDGWPWNROBNGQLGDWFVDPI KFPNGLNPLA
QQAHHHWKFCLWWEBEMITTNSQIYQQHPWWYLQYVDRTPI TARHQIVI.DISQBAW
DHLITTLINIVQNNQLDYLKWDMNRHLTQVGSTHLPAAQQGELYHRYVCGLYDILITRI
KRACFKLI I BNCSAGGGRFDFGMLPYTNQTWI SDLTDPVDRATIENGFSYLFPPRI FS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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/brotein_id="AAA25567.1"
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/brotein_id="G1:475112"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15324 ATGGCTAGTGCGCCGTTTACTTTCTTGCCAATCCTCTTAGGATTTTCAGCAACGAAGCGC 15265
                                                                                              /translation="MLLGALEAGGTKFVCATGAENGQVSDRISIPTTTVGTMTAVDD
YFTTHPVDAIGIGSFGPIGVNPHDFKYGYITTTPKFGWGDFDFLGHLKSQFNIPLYWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHITASPNAQNGRITPFETRLQLACIGQLGLELNPKQLAPSEQQLLRGALIKYQQLKS
TFIKAHFYRLPTTRHVVAWLIVTADKKQAICCYLNGLNSRVKTQHPLPLHYLDAELAY
SDSSGNRYTGHQLNTMGIPLKPTNADFTSQLIYLCQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFGVNLKMKEPFVFAAIASGIASAFLGLFHVLSVAMGPÄSVIGFISIASKSIPAFMLS
VAVSFVVAFTETTIYAKTATGODROQYSPAPFTSYTINNDBETISAPFVGASESIKQV
NDOYFSAEIMGKGAAI-TVESSDQVVAPADGVITTVTDSHHAYGIKTTAGAEILIHLGLD
TVNLNGEHFTTNVQKGDTVHQGDLLGTFDIAALKAANYDPTVMLIVTNTANYANYBANYANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="enzyme II of the PTS system, sucrose specific"/note="enzyme IIabc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 TICGGCGGCAATGAGTICCTGGGCGCCGCGTATIGGTATGGCGATGGTGTTCCCGAGCTT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AIGCATCIGCCCCGTICGCGTTCTTGCCAGTGTTGGTTGGTTTCACCGCAACCAAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 21838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 287.6; DB 1;
Pred. No. 4.3e-66;
0; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVTNVQAGEQLVALTAPAASSVAATTV"
                                                                                                                                                                                                                                                     complement (11673. .13832)
/gene="agas"
complement (11673. .13832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (13852. .15989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (13852. .15807)
/transl_table=11
product="fructokinase"
protein_id="AAA25565.1"
db_xref="GI:475110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (15872. .15877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (15894. .15989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                  GLLLAOAALKNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="scrA"
5993. .17568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="scrB"
15993. .15998
                                                                                                                                                                                                                                                                                                                                      'gene="agas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="scrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'dene="scrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="scrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 58.8
Matches 539, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein id="AAAA25563.1"
/db_xref="GI:475108"
/translation="MQEBHNYKWVGGRLIYGFGAKGNDAFYSILSGYLIIFITSHLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFTYIMGKPKSFSILSIINIFLGLIATSLFPVLSKKFSRKGVFAGCLVFMLGGIAIFT
TAGSNLMVLTAATNFGFPZQNVFLVVLMYITDSVBYGQLKLGHRDSSLALSYRPLID
KFGGAISNGVVGQIAIISGWFTAGARASITAAGQLHFKLTMFAFPALMLLIAIGIFSK
QIFLTEBKHAEIVABLERTWRTKFDNTTDQVARKVVTFBLDLAFPIAGQVIPLAQOVNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                TGNKALDNRMVSLVTLIIMVLRIVELFIDPFIGNAIDRTKNSPGHFRPWVVGGTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IILLLLFTNLGGLYAKNAMIYLVVFAILYITMDIFYSFKDVGFWSMLPSLTTDSRERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTATFARLGSTIGGGLVGVLVMPAVIFFSAKATSTGDNRGWFIFALIICLIALISAWG
VGLGTREVDSDIRKNKQDTVGVMEIFKALAKNDQLLWAALAYLFYGVGINILGSLEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFAAGTLGDGFAIKPSDGRILAPFDATVRQVFTTRHAVGLVGDNGIVLLIHIGLGTVK
LRGTGFISYVEBGQHVQQGBELLEFWDPTIKQAGLDDTVIMTVTNSTEFTMMDWLVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVGLNPKLNYQNIATKAIFGGDELMQLGFYDPVVYQDYTTKVYHFKAVTEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function="fructose 6-phosphotransferase"
                                                                                                                                                                                                                        /function="raffinose transport protein"
note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard name="terminator 3"
/note="putative"
/note="butative"
/rpt type=direct
/note="br; putative"
/rpt type=direct
/note="br; putative"
/rpt type=direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'standard name="terminator 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (10727. .11593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (10727. .11593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
evidence=experimental
                                                                                                                                                                                                                                                                        /codon_start=1
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Leenhouts, K.K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G.
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
Unpublished
                                                                                                            Direct Submission Submitted (27-APR-1994) Leenhouts K. K., Institute for Biological Sciences, Department of Genetics, Kerklaan 30, Haxen, The Netherlands, 9751 NN On May 26, 1994 this sequence version replaced gi:475962. Location/Qualifiers
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insertion element; permease; regulator; sucrase.
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Pediococcus pentosaccus
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Pediococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'function="fructose 6-phosphotransferase"
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/protein id="CAA83668.1"
/db.xref="G1475968"
/db.xref="G0A:P43470"
/db_xref="GA:P43470"
                                                                                                                                                                                                                                                                                                    'standard name="terminator
                                                                                                                                                                                                                                                                                                                                               /citation=[1]
complement(10727. .11593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (10727, .11593)
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/gene="scrA"
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/evidence=experimental
                                                                                                                                                                                                    /rpt_type=INVERTED
10681. .10716
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/transl_table=11
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58.8%;
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TILLLEFTNLGGLYAKNAMIYLVVFAILYITMDIFYSFKDVGFWSMLPSLTTDSRERE
KTATFRALGESTIGGGLVGVLVMPAVIEPSAKATSTGDNRGWEFFALLICLIALISANG
VGLGFREVDSDIRKNGDTVGVMEIFKALAKNDQLLMAALAYLFYGYGINILGSLEVY
FFTYINGKPKSBFSIRKNGDTVGVMEIFKALAKNDQLLMAALAYLFYGYGINILGSLEVY
FFTYINGKPKSBFSILAIINIFGGLATSLFPYLSKKFBSKGYPRGGLYPMLGGTAIF
IAGSNUMIVLLAATWEGFPQWVFLVVLMVITDSVEYGQLKLGHRDBSLALSVRPLID
ÇIFGGALISUVGVQQIAIISGMTTGATASSITAAGQLHFKLITMFFPFALMLLIAIGIFSK
TFAAGTLGGGFAIKPSBVTTASTDAVBKVTSLDLATPIAGQVIPP
TFAAGTLGGGFAIKPSGRILAPFDAVRQVFTTRHAVGLVGDNGITLHIGGGTVK
LRGGTGFISYVEBGGGHVQQGBELLEFWDPTIKQAGLDDTVINTTTFFTTMMDMLVKF
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YTRSVQYCVGOHAVDRETTERSCHPTLEVERTITLEGAHABREBEBRSGINYGIQT
FGSLRGTSSHQNNPFELALVDHTTERSGDA VGFNLTVSGAHABREBEBRGSINYGIQT
FGSLRGTSSHQNNPFELALVDHTTERSGDA VGFNLTVSGAHAFELEXDQLDQLALMVG
INSYNFNWQLKAGATFQTPEVLMVYTNKGLNAMSQAYHHLIRERVYRSBFROQRRPIV
VORMAZIYFFDRDAKAKFIYDBAKQATABWYLDDARFGHRDDDNSSLGDWQVDRKF
PQGLNHFVKYYHEQGILKFGTWLEPBRISSYSKLYQQHPDYLMQVPGRSPFSPROYIL
DLGRQAVRNNIFDQLDQLLKSKQIDYIKWDMNRHLSDIYSVALPPPROGEVTHRYVCI
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GLSNIQWGYRLNRSPSTISYELSRCQPYQAELAQTDAEYKRSQCGRKYKLSDELKQKI
GLNILRLSWSPGMIAHEFKLATKSIYNWLNQCRIGSLNDLPEHGYRQRRNVDQRSKYN
QSLGRSIEQRPWHYDRNRIGDFLDTVVGFRGFRGFKJTLTLIDR&SFRLMYRLKDR
TTATVNEALIKFLTTFNGFVHSFTVDRGTEFSGLNSLESQYGIKTYYCHAYTPADVVN
                                                                                                                                                                                          translation="MQEEHNYKWVGGRLIYGFGAKGNDAFYSILSGYLIIFITSHLFD"
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/translation="MSLITVDQANRVFHLHNQTLSYIPAVEQGGTLSHLYFGGHVDHY
HGELRYPRVDRGFSGNLPGSTDRTFSRDTLPKEYSTAGEMDYHLPAAIVRHTDGANAL
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AYPISLATAHVSVSPNQQTGRETSMSTRSAVAASGVLGYELDLTQLSSADKQIVQKQV
VQYKQIRPLIQFGEFYRLKSPITSNQAAWMFVSPQQDBAIVMVFNLTSYAQPSLTKTK
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(standard name="IS-element"
(citation=[1]
contact
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/protein_id="CAA83665.1"
db_xref="G1:475965"
/db_xref="GOA:p43467"
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/standard_name="terminator 3"
/citation=[1]
                                                                                                                                               xref="Swiss-Prot:P43466"
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protein_id="CAA83666.1"
db_xref="GI:475966"
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/protein_id="CAA83664.1"
|db_xref="GI:475964"
|db_xref="GOA:P43466"
|db_xref="Swiss-Prot:P434
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complement (9519.
/gene="iso-IS30"
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transl_table=11
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5976, pir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5976. .8177
/gene="agaR"
/standard_nam
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QLHAYLQEMARVLSQYDVVTVGETWCAIPEIGQMYSNPNRHELSMIFQFEQINLDKQ
SGMTRWDLKPLIPAELHAVFSKWQLALDGVGWNSLFWSNHDLPRIVSRWGDDSQYREK
SAQALAIYLHMLKGTPYIYQGEEIGMTNYPITSYHBIEDIESRRVYQQRQQGYAI"
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Dudez,A.M., Chaillou,S., Hissler,L., Stentz,R.,
Chaillou,S., Alpert,C.A. and Zagorec,M.
Physical and genetic map of the Lactobacillus sakei 23K chromosome Microbiology 148 (Pt 2), 421-431 (2002)
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Dudez,A.-M., Chaillou,S. and Zagorec,M.
Direct Submission
Submitted (20-JUL-2001) Flore Lactique et Environnement Carne, INRA, Domaine de Wilvert, Jouy-en-Josas 78350, France
Location/Qualifiers
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Lactobacillus sakei
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Lactobacillus.
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                                                                                                                                                                                                                                                                                                                          TGGTCTGCACCAGTCCTTCCCCCCAATTGAGCTGGAGCTGTT
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/db_xref="taxon:1599"
<1. .1605
/gene="scrA"
<1. .1605
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/organism="Lactobacillus
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/gene="scrA"
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Luesink, B.J., Marugg, J.D., Kuipers, O.P. and de Vos, W.M.
Characterization of the divergent sacBK and sacAR operons, involved
in sucrose utilization by Lactococcus lactis
J. Bacteriol. 181 (6), 1924-1926 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIKLEDVANKAGVSVTTVSRVINRKGYLSDATISKVEKAMODLH
YIPMAARSLOGKSIKLIGIVPPTIKNIFYAELIEKIEQALFIRGYKAMLATTEHDEG
KERDYLALLLENGVOGIISGENUKARDYIALEEPINAFELLTPETTVVSSONFEGG
ILATKALINGSSKKA AIFTGANTNEPTYLRENGYLLELERNQLKPHIIKIPSGWTLL
RKKVEIKKILENNDFDGVFCTDDLTALLVKDLASNLKKSLNVVGFDGTEFIENYYPNL
TTIKQPINDLAELLVDLIIKKIDGDNIDITYQLPVQLHYGID;"
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AGVYSGSALAFENFLFLIYTGNHRGEDWVRTPYQLGAKIDKNNQLVKFTEPLIYPDFS
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DNKLYQYPVEKMKELRQMEQDLLLADNNIITSNSYELEVDFRQQTSTILLSLMTNEKGD
SALKVEIDKENNYIITLIRNYEKRLAHVKIEKMNYFIDQSIFEIFINDGEKVLSDCRVF
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MGYMIECPNLIFINGRSVLVFCPQGLDKSIVKYDNIYPNYYJADDFTTGSKNQLKNA
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| protein id="0.2819.689.1"
| db_xref="GI-4881476"
| translation="MKWSTKQRYRTYDSYSESDLESLRKLALKSPWKSNFHIEPETGL
                                                                                                                                                                                                                                                                                                                                                                          Biophysical (NIZO), P.O.
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                                                           Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (24-JUN-1997) Luesink E.J., Department of
Chemistry, Netherlands Institute for Dairy Research
Box 20, Ede 6714 BA, THE NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..5800
/organism="Lactococcus lactis"
/mol_type="genomic DNA"
/sub_species="cremoris"
/db_xref="taxon:1388"
complement(330..1286)
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|db_xref="G1:4581475"
|db_xref="GOA:Q98685"
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Luesink, E.J.
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                                                   ACTGGCTTACATCAAAGCTTCCCGGCAATTGAAACGACACTTTTGGCAGATATTGCCAAA
                                                                                                                                                                                                          590 TGTTTGGCAGTGTTCTTCCTGGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGTGCTTCA
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                                                                                                      530 CAGGGTGGATCCTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCA
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complement (1390.

-10_signal

/gene="sacR" complement(1416. .1422)

-35_signal

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297015.1 GI:4581474 enzyme II sucrose protein; fructokinase; sacA gene; sacB gene; gene; sucrose-6-phosphate hydrolase.

Lactococcus lactis cremoris sucrose gene cluster. 297015

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BALGAINKKXPFFIALGASAIGSHPGLFHYLAVSHGSAGALIGFISTAGYTHQFM
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Pred. No. 3.3e-56;
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QRAVKGLSDIFVRIIPAIVAGGLLMGLFNVLTAPGGFIEGGSLIDANFGLADLASMIN
                                                                                                                                                                                   TFTVVGPLTRDVGFMLGDALNWLYDSAGFVGGALFGFIYAPFVITGMHHSFIAIETQL
LADIVTTGGTFIFPLAAMSTAGGAAALAVGYWTKETKLKGYAIPSGYTALLGTTEPA
MFGVNLKLRYPFIAALIGAALASAFITLFNVKAQALGAAGLPGIISINPQQIGYYIMG
MAISFVAAFALTVLLAMREKTKQAAQVTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="sucrose operon repressor SorR, putative"
/protein id="AAF96555.1"
/bxref="GI:9658078"
/bxref="GI:9658078"
/translation="WASLHDVARLAGVSKSTVSRVINDEYGVKESTKIKVLKAVEQCG
YMVNQVAKDLKSQKTNLIGVIVPRVSSHATAQGVDGLTAIFEQAGKHVLLANTHQVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / LTAIRSTAIN TO THE MALLDTLAELAGGINNVTRILAPQGOVUALKHPPLVPHLPDDVS
LQSVLGEWQLSVQRTAEVSDQQLAAIGKAIAERQKLETLPYQTALDCPYRPLWHISPP
LQSVLGEWQLSVQRTAEVSDQQLAAIGKAIAERQKLETLPYQTALDCPYRPLWHISPP
GGLLNDPWGRTYHQGBYHLFYQWHPPRCEHKDKWYHIKSLDLVDWGWGYNLJPSDW
FDSHGVFSGHAVSHQQDLWLFYGGYTRGVDRQRQTWQCAARMANGEFEKLGPVIRC
LPEGYTEHIRDPKYTYGGKRQWLLCAATLAHQGRLAYYHSDDLLHHFPKLYGDELG
DYGYMWECPDWFELGGEAFFVFGPQGIASANPHTIEHQNRIFRATQNAQGEIALLQG
NYDLGGPFYRAQTAQTAGRRVLCGWMGLAPDFTQHFSCDGWIHQLTALRELEWREG
RIYGHPLRELDTLGSEPHTLLLSDNYTELKTKSFALGVTPWGCELRLMQNTQYRYTT
TLDAENQLLKLDRSATORQGPTIRELKLDSFTVELRILADQSSLEIFINQGFHVMTS
RIFTFRDASGISLHGASVDAKLYYMAPASAPPNLEVNVQP
                                                                                                                           TFANAPFVYLPVLLAFSASKKFGGNPFLGAALGMLMVHDDLLNGWGFGSASVSGTVPT
WNILGFEIEKVGYQGSVLPVLVSAYILAKIENGLRKIVPSVVDNLLTPMLAIFITGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEIEŸIQIFNQKRYBGIVFYATHLDQPLVHAĪQHSAVPVVLVĞQDGSLYNIPSITHDD
HYGFFAGQELVKAĞCKQIGFIGVQBDIAVDYLARSQĞLQĞALĞHQQTILFHARGNF
HINSGYQMAKQAYLYPÇDLGELÇATDRLAVQAIKALQĞQKTGYQQVKLLGYGNDEL
AYVSNPPLSTFNYAFDKAĞENAAKMLLERIAGRĞQEMSKVVLTPQNIQRETCPV"
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VDLDEHGREFSFTRMYKRSADOPLQLSD1 PSPQNEMLHVSTSTALANDPSRSSTFRAIA
OMKEVGGYVS FOPPINKEBEWSEPOSLQATWKRAVGLADVVKSSEBELQFLTGTQSIEE
GLQAIADFQI PLVVVTLGAKGALVVTPNSRQIVSGKAVKPIDTTGGGDAFVGGLLYRL
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/gene="VCA0657"
/note="similar to SP:P13035 GB:M21277 GB:M55989 GB:M96795
PID:146181; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="sucrose-6-phosphate dehydrogenase"
/protein_id="AAF96556.1"
/db_xref="GI:9658071"
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sequence similarity; putative"
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/db_xref="G1:9658072"
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/transl_table=11
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/gene="VCA0654"
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'qene="VCA0654"
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'gene="VCA0655"
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                                                                                                                                                                                                                                                                                                     1365
4490 TAAATCTGGAGAACTTTTCTCACCAGCGAGGAGAATTATTATTGCTTATGAAACAGG 4549
                                                       1186 CCATGCTTTCGCAGTTCGCACCAAGGCTGAAGGTTCCAATGTGGATATCTTGATGCA 1245
                                                                                                                                                                      1246 CATTGGTTTCGACACAGTAAACCTCAACGCACGCACTTTAACCCGGTGAAGCAGGG 1305
                                                                                                                                                                                                                                 4598 TAİTİĞGAATAĞATACTĞİTTCAATGAATĞGTAATGGAİTCATACAAAATGTTAAAGTTĞĞ 4657
                                                                                                                                                                                                                                                                                                                                                          4658 CCAGAAAGTAAAAGCAGGGGATTTACTAGGATCTTTTGATAAAGAAGAAATCAAGAAGAG 4717
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Submitted (14-JUN-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 10-0CT-2003
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                                                                                                                                                                                                                                                                                            1306 CGATGAAGTCAAAGCAGGGGAGCTGCTGTGTAATTCGATATTGATGCCATTAAGGCTGC
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                                                                                                                        ---GAAGTTCTTTACA
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                                                                                                                                                                                                                                                                                                                                                                                                              1366 AGGTTATGAGGTAACCACGCCGATTGTTGTTTCGAATT 1403
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Location/Qualifiers
                                                                                                                  4550 TCACGCTTATGGTATAAAAAAAAAAATGGAGGT-
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/protein_id="AAF96554.1"
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/note="biotype: El Tor"
complement(114. .1553)
/gene="VCA0653"
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strain="N16961"
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/gene="VCA0653"
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completed: October 30, 2004, 15:50:51
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KQWQNEYDSISRLIYSGADAFSYADYHLKMASARIRTIGARMDSAFELGELANQLHI
TYQEYHQALAQONSNIQAYQATDAVBASAAERVSSHTHSAHQLIDQYQDHCAETKHSI
NVTHQULQULATQAESAALTLALSODAQOYGQLMTEIGGIREQTNILALINAAIEBAAR
AGEQGRGFAVYADEXRALSARTQRATQQIQTSIDTMLSTIEBARGDITASRDQTEQCA
QDANTTLQQLQDVBCVMSDMLRYIGBYASAAQHQRELTCEVNQHIHSIASVATQNSAA
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PROGYAPQVKNTSVMPRAMYQPRSASTEDLRQYLLSGAIQHEVVPGDFPNIKLANTVRF
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ALVQSRVAQNAIYTRGFGENVPACTNSTKNGRACNRRVEIRFILASN"
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TKSGGFYWVDAYVTPIYQQGQLIGYQSVRVKABRKWVEIATKAYQALLAABKAGKKIQ
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                                                                                                                                                                LVIINAMOROEOGAEVINYCTVEKAERNGDIMHVTILDEOTOORFERRSHALVNAAGP
WYKOPINENAHVSSPYGIRLIOGSHIIVPRIHDEPOAYILONEDKRIVFVIPYLDDYS
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DAPLPGGENFDYAALKNQLVAAFPFITESVIERWLRSYGSRTTQLLAGVTGIEDLGIA
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PFIRPAWMIRAGLFLYDNLGKRTSLPASHKVNLKAGSVTKPEMQIGFEYSDCWVDDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MYTFALIKITLEQQAEMSAYTPSAQQEVLVGDHDQLVSTTDLKG
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/protein_id="AAF96558.1"
/protein_id="AAF96558.1"
/tanslation: 19658073"
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protein id="AAF96559.1"
db_xref="GI:9658074"
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'note="identified by Glimmer2; putative"
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'protein id="AAF96560.1"
'db xref="GI:9658075"
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/gene="VCA0659"
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SUMMARIES	AAF31528 ABS65346	AAH67869	AAF32543 AAF31529	ADF / / 343_05 AAH54100 ABK73538	ACF74550 ADH84532 AAX12968	ABS98763 ABD00428 ABD00072	ABN91814 ABK73394 ABQ70786 ABQ67196 2 ABQ69245_00 ABA03041_00
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The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria,

Claim 3; Page 98-101; 144pp; English.

Abx07668 S. pneumo	Abz42306 Streptoco	Aav52334 Streptoco	Continuation (17 o	Abn66285 Streptoco	Continuation (2 of	Adh84192 Enterococ	Aas55732 Streptoco	Add13201 C. Glutam	Abz77360 Nucleotid	Aal51848 Escherich	Adf02562 Bacterial	Aag55752 Escherich	Abz42298 Streptoco	Aav52163 Streptoco	Continuation (16 o	Abk73531 Bacillus	Abn67846 Streptoco	Continuation (17 o	Abk73443 Bacillus	Abk73566 Bacillus	Aat47502 Partial P	Ach95246 Klebsiell	Abq69909 Listeria
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ALIGNMENTS

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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.
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                                                                                             Phosphoenolpyruvate; sugar phosphotransferase system; PTS;
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                                                                          C.glutamicum phosphoenolpyruvate DNA #1.
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99US-0150310P.
99DE-01042095.
99DE-01042097.
                   AAF31528 standard; DNA; 1527
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                                                                                                                Corynebacterium glutamicum.
                                                       (first entry)
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P-PSDB; ABG80325

New metabolic pathway genes of Corynebacterium glutamicum for producing fine chemicals, e.g. lipids, (un)saturated fatty acids, vitamins, cofactors or enzymes used in food, feed, cosmetics or pharmaceutical industries.

Claim 1; Page 108-111; 176pp; English

The present invention relates to the isolation of Corynebacterium glutamicum metabolic pathway (MP) proteins, and the polynucleotide sequences encoding them. The MP proteins are enzymes involved in the metabolism of molecules important for the normal functioning of cells (e.g. amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose). The polynucleotide sequences encoding the MP proteins are useful for producing fine chemicals, particularly organic acids, non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, (un) saturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes. The fine chemicals are useful in the food, animal feed, cosmetic or pharmaceutical industries. ABS65342-ABS65364 encode the C. glutamicum MP proteins of the invention

Sequence 1527 BP; 304 A; 392 C; 430 G; 401 T; 0 U; 0 Other;

ö 240 300 CGTTTCGGCGCCAATGAGTTCCTGGGCGCCGCGTATTGGTATGGCGATGGTGTTCCCGAG 120 120 180 180 240 300 360 360 480 540 540 009 099 420 420 480 600 099 9 9 CTCATGGCATCTGCGCCGTTCTTGCCAGTGTTGGTTTGGTTTCACCGCAACCAAG CTCATGGCATCTGCGCCTTCGCGTTCTTGCCAGTGTTGGTTTCTCCCCCAAG GGTTTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCAAGGCACTGC CGTTTCGGCGGCAATGAGTTCCTGGGCGCGCGTATTGGTATGGCGATGGTGTTCCCGAG CTTGGTGAACGCTACGACGTGGCCGCCACCATGGCTGCGGGCGAAATGCCAATGTGGTC GGTTTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAAGGGGCACTGC AGACTTCCTGATCACTCCAGTGCTGATTGCTGCTCACCGGGATTCCTTACATTCATCGC CATTGGCCCAGCAATGCGCTGGGTGGCGATGTGCTGGCACACGGTCTACAGGGACTTTA TGATTTCGGTGGTCCAGTCGGCGGTCTGCTTCGGTCTGGTCTACTCACCAATCGTCAT TGATTTCGGTGGTCCAGTCGGCGGTCTGCTTCGGTCTGGTCTACTCACCAATCGTCAT CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCATGTTTGGCCAGT GITCITCCTGGGAAAAGCTGAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTCTCCGC CTTGGTGAACGCTACGACGTGGCCGCCACCATGGCTGCGGGCGAAATGCCAATGTGGTC CCTGTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGTGCTGGT cerdifiredifiredarginecedadecedriaceaecedececeracineracion AGACTICCIGATCACTCCAGIGCIGACGITGCIGCTCACCGGAITCCTTACATTCATCGC CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGGTGGATC CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGGTGGATC CTTCATCTTCGCAACGCCATCTATGGCTAATATCGCCCAGGGGGGGCGCATGTTTGGCAGT GITCTICCIGGCGAAGAGTGAAAAGCICAAGGGCCTIGCAGGTGCTICAGGTGTCTCCGC Gaps 0; DB 6; Length 1527; Indels 0 100.0%; Score 1527; 100.0%; Pred. No. 0; live 0; Mismatches Best Local Similarity 100. Matches 1527; Conservative Н 61 121 301 Query Match 61 121 181 181 241 301 361 361 421 421 481 481 541 541 601 601 ð 엄 ö 셤 g Db g g g ଚ g Š δ δ g ò dd à à δ ò

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                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and identifying a nonlogue of a gene derived from coryneform corterium. Vitamins, saccharides and organic acids, nucleic acids, vitamins, saccharides and organic acids described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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la M, Ozaki A;
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Senoh A, Ikeda M,
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Tateishi N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence encodes the Brevibacterium lactofermentum sucrose
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              AGGGGAGCTGCTGTGTATTCGATATTGATGCCATTTAAGGCTGCAGGTTATGAGGTAAC
                                                               <u> Aeeegagcriecrerergaarricararicariccarraagccrecaegrirargaggraac</u>
                                                                                     CACGCCGATTGTTGTTTCGAATTACAAGAAAACCGGACCTGTAAACACTTACGGTTTGGG
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                                                                                                                               Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system; ds.
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                                                                                                                                                                                 The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS mucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotraneferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.
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Pred. No. 0;
0; Mismatches
                                                                                                                                     Page 103-104; 144pp; English
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Matches 1108; Conservative
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	Db 82160 GCAAGTTCATCTGCATTACTTGGTATTACGAACCAACCAGGATTTTTTTT	8250 TITCLACATION OF THE CONTROLL OF THE CONTR
1199 GTTCGCACCAAGGCTGAGGATGCTTCCAATGTGGATATCTTGATGCACATTGGTTTCGAC	1439 GGCGAAATTGAAGCGGGAGCCAACCTGCTCAACGTCGCAAGAAGAAGGGTGCCAGCA 1498	ADE77343 06 ADE77343 05 ADE77343 05 ADE77343 06 ADE77343 06 ADE77343 06 ADE77343 06 ADE77343 06 ADE77343 07 ADE77343 06 ADE77343 07 ADE77343 06 ADE77343 07 ADE77343 06 ADE77343 06 ADE77343 07 ADE77343 06 ADE77343 16 ADE7734 16 ADE7734

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Co epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the creatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polypurcleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the sequence continually claimes all the polypucleotide sequences given in the sequence listing of the present invention, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification, however the sequence control of the present specification of the present specification the sequence are given in the sequence of the present specification, however the sequence are given in the sequence of the present specification of the sequence specification of the present specification to the sequence specification of the sequence specification of t
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Pred. No. 1.7e-45;
0; Mismatches 364;
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ID AAH54100 standard; DNA; 2913
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physichogical provocation. Extensive follow cup characterisation is unnecessary, when one spot on an array equals one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GITICGGCGGCAAIGAGIICCIGGGCGCCGCGIAIIGGIAIGGCGAIGGIGITCCCGAGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                           Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 part of the printed specification, but was obtained in electror directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 975;
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Pred. No. 6.2e-42;
0; Mismatches 387;
                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 829; 200pp; English.
                                                                                     BIOTECH INC.
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2001US-0279526P.
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Best Local Similarity 52.6
Matches 437; Conservative
                                                                                                                                                          Clausen IG;
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                                                                                     NOVOZYMES NOVOZYMES
                   06-OCT-2000;
27-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel genes and encoded proteins from Staphylococcus arreus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein, useful as a vaccine for treating or infection, specifically an infection caused by
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preventing Staphylococcal
S. aureus, e.g. sepsis.
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P-PSDB; ABM72990.
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used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                     CTCAAGGGCACTGCAGACTTCCTGATCACTCCAGTGCTGACGTTGCTGCTCACCGGATTC
                                                                                                                                                                                                                                                                                                 227 CTTCCTGTGCTGGTGGTTTCTTGGATTCTGGCAACGATCGAGAGGTTCCTGCACAAGCGA
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                                                                                    Sequence 861 BP; 259 A; 136 C; 171 G; 295 T; 0 U; 0 Other;
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                                                                                                                              11.4%; Score 174.6; DB 8; 54.2%; Pred. No. 5.2e-41; ive 0; Mismatches 329;
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The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polymeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence
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Length 5840; Indels

Score 151.2; DB 2; Pred. No. 1.4e-33; 0; Mismatches 533;

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Conservative

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Sequence 5840 BP; 1848 A; 944 C; 1256 G; 1779 T; 0 U; 13 Other;

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19-MAR-1999

AAX12968

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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus faecalis in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by creamism, in vivo or in vitro. In particular the polypeptides encoded by prevent or attenuate an Enterococcal infection
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TIGGGIGITGITICIATIGAIGCICCAGAIAFGGICAIGTICITGGIGIGGCAGTIGIT
                                                                   869 ACCTICITCATCGCATTCGGCGCAGCGATTGCTTATGGCCTTTACTTGGTTCGCCGCAAC
                                                                                                                                      GGCAGCATTGATCCAGATGCAACCGCTGCTGCTGCTGCAGGAACGACCAAAGCCGAA
                                                                                                    2390 GCAATIGGIGCCGGAATIGCCTITAICATIGCGITIGICTIAACGITIGICTIACGII.-
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The invention describes a new isolated nucleic acid encoding a Klebsiella

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                                 vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae invention
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      ds.
                                                                                                                                                                                                                                                                                                      acid encoding a Klebsiella pneumoniae polypeptide, vaccine composition against Klebsiella pneumoniae.
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Klebsiella pneumoniae protein; antibacterial; Vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1452 BP; 256 A; 452 C; 429 G; 315 T; 0 U; 0 Other;
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51.3%; Pred. No. 1.2e-31;
tive 0; Mismatches 339; Indels
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                                                                                                                              27-JAN-2000; 2000US-00489039
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Matches 366; Conservative
                                                                                                                                                                                                                           Osborne M;
                             Klebsiella pneumoniae
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OM nucleic - nucleic search, using sw model

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7047.887 Million cell updates/sec
Title: US-09-604-231-1
Perfect score: 1527
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Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: Issued_Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 3464, Ap Sequence 2417, Ap Sequence 2417, Ap Sequence 1277, Ap Sequence 297, App Sequence 201, App Sequence 17, App 2847, Ap 30, Appl 1041, Ap 1806, Ap 1806, Ap 56, Appl 1876, Ap 1876, Ap 1837, Ap 1317, Ap 1317, Ap Description Sequence Sequence Sequence Sequence Sequence S Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-134-000C-2417 US-09-489-039A-6203 US-09-489-039A-6203 US-09-134-001C-1277 US-09-583-110-297 US-09-583-110-297 US-09-583-110-463 US-09-134-000C-2077 US-08-920-812-17 US-08-920-812-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-08-921-177-17 US-09-489-039A-1806 US-08-956-171E-56 US-09-107-532A-1876 US-09-107-532A-1876 US-09-107-532A-1876 US-08-956-171E-1317 US-08-673-190A-6 US-08-673-190A-6 US-08-673-190A-6 SUMMARIES Query Match Length 1428 30246 30246 1284 1887 143.6 1126.6 1126.6 1126.6 1117.6 1114.6 1109.6 1109.6 1109.6 1109.7 1109.7 1109.8 86.2 86.2 83.2 81 Result Ņ.

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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION UNDER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
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51.3%; Pred. No. 7.9e-34;
live 0; Mismatches 339;
                                                                                                               Sequence 5847, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NEDWONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1090-01.29
PRIOR FILING DATE: 1999-01.29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6203
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Best Local Similarity 51.3%; Pred. No. 7.7e-34;
Matches 366; Conservative 0; Mismatches 339;
                                                                                                  Sequence 6203, Application US/09489039A
Patent No. 6610836
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877 422 937 482

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APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 1000-05-26
PRIOR PLING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
NUMBER: OS 60/051,553
PRIOR FILING DATE: 1993-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NOS: 5322
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Pred. No. 1.7e-28;
0; Mismatches 629;
       ; Sequence 297, Application US/09583110
; Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA; TYPE: DNA; ORGANISM: Streptococcus pneumoniae US-09-583-110-297
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Best Local Similarity 47.0%;
Matches 581; Conservative
                                                                      GENERAL INFORMATION:
JS-09-583-110-297
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                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION WUMBER: US/99/134,001C
CURRENT APPLICATION WUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
SEQ ID NOS: 5674
LENGTH: 732
LENGTH: 732
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; CTHER INFORMATION: Identity of nucleotide at the above locations are US-09-134-001C-1277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 732;
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Pred. No. 4.2e-32;
0; Mismatches 221;
                                                                        Sequence 1277, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAGTCCTTCCCGCCAATTGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Staphylococcus epidermidis
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cal Similarity 56.4%;
305; Conservative
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US-08-961-527-201
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
UNMER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
rgcrc----rigacirrcrrcrriccaaggcrgrcrcrcacaaaaragggggg 1435
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                                         TCGGCGCAGCGATTGCTTATGGCCTTTATTGGTTCGCCGCAACGGCAGCATTGATCCAG
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Genome Sciences, Inc
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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Patent No. 6420135
GENERAL INFORMATION:
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CITY: Rockville
STATE: Maryland
COUNTRY: USA
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APPLICATION NUMBER: US/(
CLASSOFT-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 126.6; DB 4; Length 3895;
Pred. No. 2.6e-28;
0; Mismatches 619; Indels 27;
                                                                      201:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%;
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 20.
SEQUENCE CHARACTERISTICS:
LENGTH: 3895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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509 AITGAGCIGGAGCIGITTAACCAGGIGGAUCCTICAICTICGCAACGCCAICIAIG 565	566 GCTAATATCGCCCAGGGTGCGGCATGTTTGGCAGTGTTCTTCCTGGCGAAGAGTGAAAAG 625	626 CICAAGGGCCIIGCAGGTGCIICCCGCIGTTCTTGGTAITACGGAGCCTGCG 685	686 AICTFOGGIGTGAACCTTCGCCTGGCCGTTCTTCATCGGTACCGCAGCT 745	746 AICGGIGGCGCTTIGATIGCACTCTITAATAICAAGCACTTGCGTIGGGCGCTGCAGGI 805	806 TICTIGGGIGTIGTITCIANIGANGCICCAGATANGGICATGTTCTIGGIGTGNGCAGTT 865 1240 AICCCIGGNCAANGCITTANGTIGGNAACGGACAACTICCACAANACCTICTTANGGNA 1299	866 GTTACCTTCTTCATCGCCACTGCGATTGCCTTATGGCCTTTACTTGGTTCGCCG 925	926 AACGGCAGCATTGATCCAGATGCAACCGCTGCTCCCAGTGCCTGCAGGAACGACCAAAGCC 985	986 GAAGCAGAAAGCACCCGGAGAATTTTCAAACGATTCCACCATCATCCAGGCACCTTTGACC 1045	1046 GGTGAAGCTATTGCACTGAGCGTCAGCGATGCCATGTTTGCCAGCGAAAGCTTGGC 1105	1106 TCGGGCGTTGCCATCGTCCCAACGGGCAGTTAGTTTCTCCGGTGAGTGGAAAGATT 1165	GIGGIGGCATTCCCATCIGGCCATGCTTTCGCAGTTCGCACCAAGGCTGAGGAIGGTTCC 122.		1286 AACCGGTGAAGAAGCAGGGGATGAAGTCAAAGCAGGGGGGGCTGTGTGAATTGGAT 1345 1687 GAAGCAAAAGTTGCTCAAGGTAATAAGGTGAAAGGTGGCGATGTTCTTGGAACATTTGAC 1746	1346 ATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACCACGCCGATTGTTTCGAATTAC 1405 1747 TCAAACAAAATCGCTGCAGCTGGACTTGATGATACAACAATGGTTATCGTTACGTAACAAAATCGTTAACAAAAATCGTTAATGATACAACAAAAAATGGTTAACAAAAAAAA	1406 AAGAAAACCGGAACTGTAAACATTTAGGCGAAATTGAAGGGGGGAGCCAACTG 1465 1807 GCTGACTACGCTTCAGTAGCTCCAGTGGCAACAGGTTCAGTTGCGAAAGGGGATGCTGTG 1866	1466 CTCAACGTCGCAAAGAAA 1483 	RESULT 9 US-09-134-000C-2077 ; Sequence 2077, Application US/09134000C ; Patent No. 6617156
Sy da	\$ B	čo qa	λζ qq	Å qa	VQ DP	ý g	S S	Qy Dp	රු අ	č d	QY Pb	S d	음 당	QV QD	QY Db	da da	RESI US-I SC
QY 1081 CATGITIGCCAGCGGAAAGCITGGCTCGGGCGTTGCCATCGTCCCAACCAAGGGCAGTT 1140 Db 2324 TAITITGCATCAGGTGTCATGGGCAAGGTCTAGTCATTGAACCAAGCCAAGGTGAGTT 2265	OY 1141 AGTITCTCCGGTGAGAGATTGTGGTGGCATTCCCATCTGGCCATGCTTTCGCAGT 1200 Db 2264 GACCTCTCCAGTTAATGGGACAGTGACGTTCTTTTCCCTACCAAGCATGCCATCGGCAT 2205	OY 1201 TCGCACCAAGGCTGAGGATGCTTCCAATGTGATATCTTGATGCACATTGGTTTCGACAC 1260 Db 2204 TGTCTCTGACGAGGAGTTGAATTGCTCATCCACATCGGTATGGATAC 2157	OY 1261 AGTARACCTCAACGGCACGCACGCTGAAGAAGCAGGGCGATGAAGTCAAAGC 1320 Db 2156 AGTAGGCTTGATGGCAAGGTTTTGAAAGTCTTGTAGTCCAAGGAGATCACGTTACAGT 2097	Oy 1321 AGGGGAGCTGCTGTGTGGATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAAC 1380 Db 2096 TGGTCAGCAACTGATTCGTTTTGATATGGATGTCATTAAGGCTGCAGGTCTGCAGGTAAGA 2037	OY 1381 CACGCCATTGTTTCGAA 1401	RESULT 8 US-09-583-110-463	; Sequence 463, Application US/09583110 ; Patent No. 6699703 ; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al.	Nucleic Acid a Pneumoniae for TH00-07A	; CURRENT FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: US 09/107,433 ; PRIOR FILING DATE: 1998-06-30 ; PRIOR APPLICATION NUMBER: US 60/085,131	; PRIOR FILING DATE: 1998-05-12 ; PRIOR APPLICATION NUMBER: US 60/051,553 ; PRIOR FILING DATE: 1997-07-02 ; NUMBER OF SEQ ID NOS: 5322	; SEQ ID NO 463 ; LENGTH: 1884 ; TYPE: DNA ; ORGANISM: Streptococcus pneumoniae US.09-583-110-463	Query Match Query Match Rest Local Similarity 46.4%; Pred. No. 1e-25. Matches 503. Conservative 0. Mismatches 640. Indels 36. Gans 5:	GGCACCGTGCTTCCTGGTGGTTCTTGGATTCTGGGAACGATCGAG 26	269 AAGTTCCTGCACAAGCGACTCAAGGGCACTGCAGACTTCCTGATCACTGCTGACGCTGACGCTGACGCTGACGTGACTTCCTGATCACTGCTGACGTGACTTCCTGATCACTGATGACTGCTGACGTGACTGAC	700 AAAGCIGICCGCAAGSTIGITCCAGAISICATIGACCICTIGGIAACACCATICGIAACA 329 TIGCIGCTCACCGGAITCCTTACATICGCCCATICGCCCAGCAAIGCGCTGGGTGGGC	Db 760 CTITIGGTCATGTCTAGGACTCTTTGTCATTGGACCAGTTTTCCACGTTGTTGAA 819 Qy 389 GATGTGCTGGCACACGGTCTACAGGGACTTTATGATTTCGGTGGTCCAGTCGGGGGTCTG 448 Db 820 AACTACATCTTATTGCTACAAAGCGATTCTTAGCATTGGTCTTGGTGTTTC 879	449 880

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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 540; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid_
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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APPLICANT: Ohno,
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MOLECULE TYPE: GE
ORIGINAL SOURCE:
                                                                                                                                                                                                                          RESULT 10
US-08-920-812-17/c
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Best Local (
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                   APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BNTENCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENT NOS: 6812
LENGTH: 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1004 GAATTITCAAACGATTCCACCATCATCCAGGCA---CCTTTGACCGGTGAAGCTATTGCA 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTATGAATCACGTGAAAAACTTTACGTTTGGCTTGGTTAGTATGTTGAGCTTGCCTGGC 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.5%; Score 114.6; DB 4; Length 951; Best Local Similarity 48.4%; Pred. No. 5.5e-25; Matches 429; Conservative 0; Mismatches 434; Indels 24
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecalis
US-09-134-000C-2077
SENERAL INFORMATION:
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1301 CAGGGCGATGAAGTCAAAGCAGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAG 1360
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                                                 769 CAAGGTGATTCTGTTAAAAAGGAGATTTGCTAGTTACTTTTGATATTGCTGCCATTAAA 828
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                                                                                                        1361 GCTGCAGGTTATGAGGTAACCACGCCGATTGTTGTTTCGAATTACAA 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 3615;
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Welara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                             829 GAAGCTGGTTATCCGGTAGTTACACCGATTGTGGTAACGAATACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606-0+0.c

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812

WITHING DATE: 29-AUG-1997
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Similarity 46.3%; Pred. No. 4.4e-23;
10; Conservative 0; Mismatches 589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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APPLICATION NUMBER: US 08/362,577
ETLING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08920812
Patent No. 5763188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia coli; STRAIN: Clinical Isolate EC-24 US-08-920-812-17
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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RESULT 11 US-08-920-827-17/c

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                                                           APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  Borun
                                                                                                                                                                                                                                                  Gerstein, Murray &
South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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Pred. No. 4.4e-23;
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FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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STRAIN: Clinical Isolate EC-24
Sequence 17, Application US/08920827
                                                                                                                                                                                                                                               3: Marshall, O'Toole,
6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,547
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rin-Laures, Li-Hsien
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
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Best Local Similarity 46.3's
Matches 540; Conservative
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STRANDEDNESS: double
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APPLICATION NUMBER: U
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                          Patent No. 5770375
GENERAL INFORMATION:
APPLICANT: Obno, 7
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                                                                                                                                                                                                                                                       ADDRESSEE:
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US-08-920-827-17
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                   6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                         Version #1.25
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
                                          CITY: Chlcay-STATE: Illinois
COUNTRY: United States of America
7TP: 6060-6402
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
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STRAIN: Clinical Isolate EC-24
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REFERENCE/DOCKET NUMBER: 1903
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 540; Conservative
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STRANDEDNESS: double
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Patent No. 5798211
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsunisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Bda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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CGTTGGGCGCTGCAGGTTTCTTGGGTGTTGTTTCTATTGATGCTCCAGATATGGTCATGT
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APPLICANT: Otho, Tsuneya
APPLICANT: Otho, Tsuneya
APPLICANT: Uchara, Hirotsugu
APPLICANT: Uchara, Hirotsugu
APPLICANT: Dear Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDEMES: 25
CORRESPONDEMES: APPLICANT: ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ZIP: 60606-6402
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; Sequence 17, Application US/08362577C
; Patent No. 5807673
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                     NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMUNICATION INFORMATION:
TELEPHOME: 312/474-6300
TELEPRAX: 312/474-0448
US/08/362,577C
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; STRAIN: Clinical Isolate EC-24
US-08-362-577C-17
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                                                                 27-MAR-1995
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
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APPLICATION NUMBER:
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STRANDEDNESS: doub
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                                                                                 FILING DATE: 27
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TELEX: 25
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ORIGINAL SOURCE:
                                                                                                                                                       TOPOLOGY: 11 MOLECULE TYPE:
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
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COUNTRY: United States of America
ZIE: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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Patent No. 585398
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Wetsuhisa, Akio
APPLICANT: Bac, Soji
TITLE OF INVENTION: Probe for Diagn
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Get
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APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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STREET: 62...
TTV: Chicago
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Pred. No. 4.4e-23;
0; Mismatches 589;
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STRAIN: Clinical Isolate EC-24
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Best Local Similarity 46.3%;
Matches 540; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Patent No. 6605709
GENERAL INFORMATION:
PAPLICATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
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410; Conservative
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| cgm2_6/ptodata/1/pubpna/US06_DNEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Semience 9 Appli	Segmence 1. Appli	Segmence 2904. An	Semience 829	Segmence 31 Appl	Segmence 685, App	Semience 3599 An	Semilare 9 Amili	Semience 2058 An	Semiance 160 ann	Semience 201 Ann	Sequence 201, App
		E .	100.0 1527 16 US-10-450-055-9	9 US-09-738-626-1	US-09-738-626-2904	US-09-974-300-829	US-09-070-927A-31	US-09-974-300-685	16 US-10-398-221-3599	6 US-10-398-221-9	16 US-10-398-221-2058	17 US-10-474-776-160	US-08-961-527-201	6 US-10-158-844-201
		Match Length DB ID	1527 1	3309400	1983 9	975 9	5840 9	1380 9	8.9 3037 1	684707 1	3011208	2127 1	3895 8	3895 1
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US-09-815-242-9369		US-08-961-527-30	US-10-158-84	US-09-974-	US-09-974-300-734	US-09-974-300-85	US-10-398-221-	6 US-10-398-221-2722			US-08-781-98	US-1		6 US-10-398-221-2857	US-10-398-221-388	US-09-974-300-877	US-09-974-300-893	Þ		₽	5 US-10-282-122A-21444		5 US-10-282-122A-36728	US-09-070		US-09-974	5 US-10-282-122A-39556	US-09-974	US-10-28	7 US-10-474-776-65	US-08-961-527-16	US-10-158-844-163
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113.4	107.8	107.8	107.8	105.6	9 9	86	93.6	93.6	93.6	87.8	86.2	86.2	81.6	81.6	78.8	77.4	76.8	76.4	76.4	74.2	73.2	72.4	72.4	70.4	69.8	69.4	69.2	68.2	67.2	67	67	67
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ALIGNMENTS

us-09-604-231-1.rnpb

Db 1201 TCGCACCAAGGCTGAGGATGCTTCAATGTGGATATCTTGATGCACTTCGACAC 1260 Qy 1261 AGTAAACCTCAACGGCACGCACTTAACCCGCTGAAGAGCAGGCGATGAAGTCAAAGC 1320 1261 AGTAAACCTCAACGGCACGCTTTAACCCGCTGAAGAGCAGGCGATGAAGTCAAAGC 1320 Qy 1321 AGGGGAGCTGCTGTGAATTCGATATTGATGCATTAAGGGCGATATGAGGTAAC 1380 Db 1321 AGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTAAC 1380 Qy 1381 CACGCCGATTGTTGTTTCGATTATCAAGACCTGCAAAGACTGCAGGTAAC 1380 Qy 1381 CACGCCGATTGTTTCGAATTACAAGAACCGGACCTGTAAAGACTTTACAGGTTATGGG 1440 Db 1381 CACGCCGATTGTTTTCGAATTACAAGAAACCGGACCTGTAAAACACTTACGGTTTTGGG 1440 Qy 1441 CGAAATTGAAGCGGGAGCCAACCTGCCAAAGAAAGAAAGA	RESULT
	481 CACTGGTCTTGCACCAGTCCTTCCCGCAATTGAGCTGGAGCTGTTTAACCAGGTGGATC 540 481 CACTGGTCTTCCAGCAGTCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGTGGATC 540 481 CACTGGTCTGCACCAGTCCTTCCGCCAATTGAGCTGAGGTCTTTAACCAGGTGGATC 540 541 CTTCTTCCTGCAGCAGGCATCTATGGCTAATTGACCAGGGGATGTTTGAGCTGGAGCTGTTTGAGGTGTTGAGGTGTTGAGGTGTTGAGGTGTTGAGGTGTTGAGGTGTGTGAGGTGTTTGAGGTGTGTGAGGTGTTTGAGGTGTGTGAGGTGTTGAGGTGTGAGGGTGTGAGGTGTGAGGGTGTGAGGTGTGAGGGTGTGAGGGTGTGAGGGTGGT

Db 2810067 AGTAAACCTCAACGGCACGTTTAACCGGTGAAGAAGCAGGGGATGAAGTCAAAGC 2810008 Qy 1321 AGGGAGCTGCTGTGTAATTGATTTGATGCCATTAAGGCTGCAGGTTATGAGGTAC 1380 Db 2810007 AGGGAGCTGCTGTGAATTTGATATTGATGCCATTAAGGCTGCAGGTTATGAGTAC 2809948 Qy 1381 CACGCGATTGTTGAATTTGATATGAGACTGCAGGTTATGAGGTAC 2809948 Qy 1381 CACGCGATTGTTGTTTTCGAATTACAAGAACCGGACTGTAACGGTTATGGG 1440 Db 2809947 CACGCCGATTGTTGTTTTCGAATTACAAGAACCGGACTGTAAACACTTTACGG 2809888 Qy 1411 CGAAATTGAAGCGGAGCCAACCTGCTCAACGTCGCAAAGAAAG	RESULT 3 US-09-738-626-2904 Sequence 2904, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION: APPLICANT: NAKAGAWA, SATOSHI APPLICANT: NAKAGAWA, SATOSHI APPLICANT: HAYASHI, MIKIRO APPLICANT: TATEISHI, MAKON APPLICANT: YOKOI, HARUHIKO APPLICANT: YOKOI, HARUHIKO APPLICANT: YOKOI, HARUHIKO APPLICANT: SENCH, AKIHIRO APPLICANT: SENCH, AKIHIRO APPLICANT: SENCH, ANDOKO APPLICA	SEG TWARE Patentin ver. 3.0
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                                                                                                                Length 5840;
                                                                                                       Score 151.2; DB 9;
Pred. No. 8.5e-36;
0; Mismatches 533;
            ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-070-927A-31
                                                                                                       9.9%;
                                                                                                                                    Best Local Similarity 48.5
Matches 525, Conservative
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION PATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
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REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
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FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
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Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
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SEQUENCE CHARACTERISTICS:
LENGTH: 5840 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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 2789 GAATTATCAGTGAAACAAGGTGATTCTGTTAAAAAAGGAGATTTGCTAGTTACTTTTGAT 2848
                                    ATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACCACGCCGATTGTTTGGAATTAC 1405
                                                                   2849 ATTGCTGCCATTAAAGAAGCTGGTTATCCGGTAGTTACACCGATTGTGGTAACGAATACG 2908
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                                                                                                                                                                                                              ; Sequence 665, Application US/09974300
; Patent No. US2020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT PILICATION NUMBER: 09/680,598
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR PLICATION NUMBER: 60/279,526
; PRIOR PLICATION NUMBER: 60/279,526
; PRIOR PLICATION NUMBER: 60/279,526
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Pred. No. 1e-31;
0; Mismatches 273;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bacillus licheniformis US-09-974-300-685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.0%;
Best Local Similarity 53.2%;
Matches 314; Conservative
                                                                                                                                 AA 2910
                                                                                                       AA 1407
                                                                                                                                                                                      RESULT 6
US-09-974-300-685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1380
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AACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCATGTTTGGCAGTGTTCTTCCTGGC 612
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT PILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
                                                          746 ATCGGTGGCGCTTTGATTGCACTCTTTAATATCAAGGCAGTTGCGTTGGG
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, OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3599
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Pred. No. 5.4e-31;
                                                                                                                                                                                                                                                            Sequence 3599, Application US/10398221
; publication No. US20040018514A1
; GENERAL INFORMATION:
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SEQ ID NO 3599
LENGTH: 3037
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Best Local Similarity 48.3
Matches 539; Conservative
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                                                                                                                                                ATCTAACACAGTAGAAGGCGAAAC------TTTAATCGAACGTGAAACAATTCC 1370
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                                                       CTTGGTTCGCCGCAACGGCAGTTGATCCAGATGCAACCGCTGCTCCAGTGCCTGCAGG
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US-10-398-221-9/c
| Sequence 9, Application US/10398221
| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: GLASER, Philippe
| TITLE OF INVENTION: Listeria innocua, genome and applications
| TITLE REFERENCE: 344 702 - US
| CURRENT APPLICATION NUMBER: US/10/398,221
| CURRENT FILING DATE: 2003-03-27
| PRIOR FILING DATE: 2001-10-04
| PRIOR FILING DATE: 2001-10-04
| PRIOR FILING DATE: 2001-10-04
| PRIOR FILING DATE: 2001-10-04
| NUMBER OF SEQ ID NOS: 4025
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 9
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8.8%; Score 134.6; DB 16; Length
Best Local Similarity 48.2%; Pred. No. 1.3e-29;
Matches 537; Conservative 0; Mismatches 534; Indels
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NAME/KEY: misc feature

LOCATION: (1)...(end)

OTHER INFORMATION: n can be any nucleotide: a, US-10-398-221-9
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ORGANISM: Listeria innocua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACTGTCGGACGCGTTGTAGCTCCAGCAGCAGCAGTAACAACTATCTTCCCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19595 GCGATGTAATCGAAAAGGTCAATTACTAACTGAATTTGATATTGAAGGCATTAAAGCAG
                                                                                                                                                                                   29307 AAACTITAATCGAACGTGAGACAATTCCAGCTCCAGTAGTTGGCGAAATCGTAACTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACCAAGGGGCAGTTAGTTTCTCCGGTGAGAAAGATTGTGGTGGCATTCCCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1185 GCCATGCTTTCGCAGTTCGCACCAAGGCTGAGGATGCTTCCAATGTGGATATCTTGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATTGGTTTCGACACACACATCAACGGCACGCACTTTAACCCGCTGAAGAAGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGATGAAGTCAAAGCAGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTG
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                                                                                       AATTITCAAACGATTCCACCATCATCCAGGCACCTTTGACCGGGGAAGCTATTGCACTGA
                                                                                                                                                                                                                                                                               1065 GCAGCGTCAGCGATGCCATGTTTGCCAGCGGAAAGCTTGGCTCGGGCGTTGCCATCGTCC
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Pred. No. 2.6e-28;
0; Mismatches 619; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29715 TGATTACAGATGCAAAAGAAGCTAAACTAGAAG 29747
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         29268 CTGAAGCAGTTGTAGAAGAAACTAACGTAA-
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; ORGANISM: Streptococcus pneumoniae
US-10-474-776-160
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Best Local Similarity 47.1%;
Matches 575; Conservative
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US-10-474-776-160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28674 tractrirccingnaarcesaccaarcesaacrissecresarriacirissaccassia 28733
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                                                                                                                                                                                                                         US-10-398-221-2058
US-10-398-221-2058
US-10-398-221-2058
US-10-398-221-2058
US-10-398-221-2058
US-10-2058, Application US/10398221
PUblication No. US20040018514A1
GENERAL INFORMATION:
TITLE OF INVENTION: Listeria innocua, genome and applications
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT TILING DATE: 2003-27
FRICR APPLICATION NUMBER: PCT/FR 01/03 061
PRICR FILING DATE: 2001-10-04
PRICR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 4025
SEQ ID NO 2058
LENGTH: 3011208
LENGTH: 3011208
CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINED TO CONTAINE
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48.2%; Pred. No. 2.6e-29;
tive 0; Mismatches 534; Indels
                   239891 TGATTACAGATGCAAAGAGCTAAACTAGAAG 239859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: L1ST
US-10-398-221-2058
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Publication No. US20020033233A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INPORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3895 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                     STATE: Maryland
COUNTRY: USA
ZIP: 20850
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                                                                                                                                                                                   .257 TİTCAİĞCATCGCCAİĞATGAĞCGTGAĞĞCTCAGGİTTCACTİCCİGCAACCAİTİCAĞ 1316
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                                            1077 AGTTAAATGGCTCTTCGGTGCAATTTTTGGCGCCCTCTACGCTCCATTTGTCATCACAGG
                                                                                                                       CGGTGGTCCAGTCGGGTCTGCTTTCGGTCTGGTCTACTCACCAATCGTCATCACTGG
                                                                                   TCTGCACCAGTCCTTCCCGCCAATTGAGCTGAGCTGTTT---AACCAGGTGGATCCTT
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              DB 8; Length 3895;
Query Match
8.3%; Score 126.6; DB 8;
Best Local Similarity 47.1%; Pred. No. 3.4e-28;
Matches 575; Conservative 0; Mismatches 619;
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RESULT 11 US-08-961-527-201/c ; Sequence 201, Application US/08961527

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126.6; DB 16;
Pred. No. 3.4e-28;
0; Mismatches 619;
                                                                                                                                                                                                                                                          NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB340F1D1
                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
                                                                                                                                                                                             60/029,960
                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 201:
SYSTEM: Windows
                                                                                  FILING DATE: 03-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                     FILING DATE: 1997-10-30
APPLICATION NUMBER: US 6
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3895 base pairs
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 201:
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                          SOFTWARE: ASCII Text
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ilarity 47.1%;
Conservative
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Best Local Similarity
Matches 575; Conserv
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MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
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TITLE OF INVENTION: STREPTOCOCCUS
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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Pred. No. 3.3e-24;
0; Mismatches 601;
                  FastSEQ for Windows Version 4.0
                                                                           TYPE: DNA ORGANISM: Streptococcus pneumoniae
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Best Local Similarity 46.8%;
Matches 560; Conservative
                                                                                                                                                                  .. (1884)
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US-09-815-242-9369
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APPLICANT: Haselbock, Robert
APPLICANT: Oblsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
ITLE OF INVENTION: Identification of Essential Genes in
TITLE OP INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-3
PRIOR FILING DATE: 2000-01-3
PRIOR FILING DATE: 2000-01-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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Patent No. US20020061569A1
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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CITY: Rockville
STATE: Maryland
COUNTRY: USA
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TITLE OF INVENTION: NOVEL STREPTOCOCCUG PNEUMONIAE OPEN READING FRAMES ENCODING POLYE
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AMIO0649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT APPLICATION DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
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Pred. No. 1.5e-22;
0; Mismatches 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 152, Application US/10474776; Publication No. US20040110181A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Streptococcus pneumoniae
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al Similarity 46.6%;
552; Conservative
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Best Local Similarity
Matches 552; Conserv
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US-10-474-776-152
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LENGTH: 1185
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                                                                                                       ##FILLED DATE:
ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
RAGISTATION UNDER: 36,373
REFERENCE/DOCKET NUMBER: BB340P1
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 30;
SEQUENCE CHARACTERISTICS:
LENGRIF: 9769 base pairs
TYPE: mucleic acid
STRANDENESS: double
"NOTINGY: linear
CURRENT APPLICATION DATA:
                              APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-961-527-30
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1019 TCCACCATCCAGGCACCTTTGACCGGTGAAGCTATTGCACTGAGCAGCGTCAGCGAT 1078
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                                                                   8277 Gaaácacirei---aacicciaicgicágicálichicíccicirgengaichcianga
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Job time : 760 secs
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BQ993574 QGF4810.1 BQ991717 QGF234724 BQ981717 QGF234724 BQ986791 QGF16003. BQ995038 QGF8003.7 BQ995038 QGF8003.7 AL065923 Drosophil AL238306 Tetraodon AL078875 Drosophil AL243904 Tetraodon CC366418 PUHEW79TB CC366418 PUHEW79TB CC366418 PUHEW79TB CC3657957 EST429680 CF753589 EST-Conti

QGF15A22. QGF10N14. QGF4e10.y QGF23J24. QGF15O03.

604169160

BU345319 BQ988486 BQ986937

EST48225

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PUBERGÉTD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa035K11,
BZ685850
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Sae mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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CL661694 PR.1013c
CC61694 PR.1013c
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                    /note="Vector: pEpifos-5 Fosmid
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Veterinary Blomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 10
Emall: j.hopkins@ed.ac.uk
Plate: 04 row: M column: 09
Seq primer: Ml3reverse
High quality sequence stop: 547.
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/db_xref="taxon:9940"
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1 (bases 1 to 770)
Gossmar-A. and Hopkins, J.
Ovine spleen\brain cDNA library
Unpublished (2004)
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/mol_type="genomic DNA"
/strain="California"
/db xref="taxon:54126"
/clone_lib="Nixed stage fosmid library of P. pacificus
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Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

1 (bases 1 to 750)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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                                                                                                                       CTTGGTGAACGGCTACGACGTGGCCGCCACCATGCCGAGCGGAAATGCCAATGTGGTC
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Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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CL686986
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P037-3-E04.za Ppa EcoRI BAC Library Pristionchus pacificus genomic, GCCA.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.A.O.C.A.O.C.A.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.A.O.C.
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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var. California"
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/strain="california"
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Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                         Length 861;
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                                                                                                                                                                                                                                                                         /note="Vector: pEpifos-5 Fosmid vector"
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601391
Email: ralf.sommer@tuebingen.mpg.de
                                                                                   pacificus"
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                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                               Score 73.2; DB 9;
Pred. No. 2.3e-09;
                                                                                   /organism="Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1453 GGGAGCCAACCTGCTCAACGTC 1474
                         Location/Qualifiers
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Pristionchus pacificus
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Best Local Similarity 55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            144; Conservative
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PRI0129d_H09 - PRI0129d_B21 (861) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificabas

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Bvolutionary Biology

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Speamannstr. 37-39, Tuebingen D-72076, Germany

Fax: 00497071601391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CCTGTTTGGT-----TTAGATGTTGCCCAAGCCGGTTACCAGGCACCGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 ICCICIGIGGIGGITICITGGAITCIGGCAACGAICGAGAAGITCCIGCACAAGCGACI
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Neodiplogasteridae, Pristionchus.
/clone_lib="Sheep spleen\brain pSport1 library"
                                                                                                   Length 770;
                                                                                                                                                               Indels
                                                                                            Score 80.8; DB 7; Pred. No. 1.4e-11; 0; Mismatches 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 ACCAATCGTCATCACTGGTCTGCACCAGTCCTTC 502
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This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CL657583
CL657583.1 GI:50139334
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Pristionchus pacificus
                                                                                      Query Match 5.3%;
Best Local Similarity 50.4%;
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        survey sequence.
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CL657583
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Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Hordeum.

El (bases I to 680)

Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.

EST sequencing and analysis in barley

Unpublished (2000)

Contact: Michalek W

Institute for Plant Genetics and Crop Plant Research

Contact: Michalek@ibk-gatersleben. Germany

Email: michalek@ibk-gatersleben.de, http://pgrc.ipk-gatersleben.de

Seq primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL506262 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare subsp. vulgare cDNA clone HY02I24T 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1409 AAAACCGGACCTGTAAACACTTACGGTTTGGGCGAAATTGAAGCGGGAGCCAACCTGCTC 1468
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                                                                                                                                                                                                                     P. pacificus
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This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

Seq primer: T7

Class: formid ends.

1. 788

/ Organism="Pristionchus pacificus"
//mol type="genomic DNA"
/ strain="California"
/ db xref="texxon:54126"
/ clone lib="Mixed stage fosmid library of P. pacificus"
/ var. California"
/ note="Vector: pBpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caryopsis (3.-15.DAP)"
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                                                                                                                                                                                                                                                                                                                           Score 62; DB 9; Length 788
Pred. No. 3.8e-06;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol type="maxx" /cultivar="barke" /cultivar="barke" /db species="vulgare" /db xref="taxon:112509" /clone="HY02124T" /tissue type="developing ci/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare subsp. vulgare
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llarity 52.3%;
Conservative
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Matches 137; Conserv
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PRI0162a D06_2 - PRI0162a.BR (788) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
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Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Meodiplogasteridae; Pristionchus.
1 (bases, 1 to 788)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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                                                                                                                                                                                                            292 GGGCACTGCAGACTTCCTGATCACTCCAGTGCTGACGTTGCTGCTCACCGGATTCCTTAC
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                                                                                      Length 1412;
                                                                                    Score 63.2; DB 9; Length 1
Pred. No. 2.1e-06;
0; Mismatches 308; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-19, Tuebingen D-72076, Germany
Tel: 00497071601371
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Email: ralf.sommer@tuebingen.mpg.de
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CL693618
CL693618.1 GI:50215526
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                                                                                             4.1%;
                                                                                                                                  Conservative
                            vector."
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nes 274; Conserv
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Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisle:
AppaDB: an AcedB database for the nematode:
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
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This library was generated at Caltech,
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/note="Wetcr: plasmid pBK-CWV, Site 1: EcoRI; Site 2: Xho1; mRNA was made from developing caryopsis (3.-15_DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"
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Neodiplogasteridae, Pristionchus.
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    763
/organism="Pristionchus pacificus"

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Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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0
CL695497.1 GI:50217405
                                   Pristionchus pacificus
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Best Local Similarity 45.6%;
Matches 247; Conservative
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PRI016c_C08_2 - PRI016c.BR (763) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic curvey sequence.
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אסט 1328 bp DNA linear GSS 17-DBC-2002 msh2_2811.x3 msh Pseudomonas aeruginosa genomic clone msh2_2811, באפולסטחור survey sequence.
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                                                                                                                                                  Pseudomonas aeruginosa
Bacteria, Proteobacteria, Gammaproteobacteria; Pseudomonadales,
Pseudomonadaces; Pseudomonas.

1 (bases 1 to 1328)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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/clone="msh2_2811"
/clone | lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library."
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Best Local Similarity 49.2%; Pred. No. 0.074;
Matches 163; Conservative 0; Mismatches 156; Indels 12;
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/mol type="genomic DNA"
/strain="MSH"
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University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                       craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Contact: Chris K. Raymond
                                                                                                 BZ572810.1 GI:27207871
                                                                                                                                          Pseudomonas aeruginosa
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Email: craymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1207
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   Neodiplogasteridae; Pristionchus.

(bases 1 to 763)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
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Pred. No. 0.12;
); Mismatches 286; Indels
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var. California"
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Max-Planck-Institute for Developmental Biology
Max-planck-Institute for Developmental
May-Planck-Institute for Developmental
Tel: 00497071601371
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RESULT 11 T03017/c

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE PUBMED

COMMENT

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/clome_lib="pistil, 1 DPA, no treatment, cv Optic, EBpi01"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Porlived from pistils dissected from developing grains (24
hours post anthesis) in glasshouse grown barley plants.
Developed as part of the barley transcriptome resources of Panalism of the barley transcriptome resources of Panalism of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the pa
                        BST.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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PRI013c_B10 - PRI013c.B21 (791) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
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                                                                                                                                                                                                                                             Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Card Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
On Nov 21, 2001, this sequence version replaced gi:17031891. Contact: Waugh R, Marshall DF Genome Dynamics/Computational Biology
                                                                                                                                                       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
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/mol_type="mRNA"
/multivar="Cptic"
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/clone="RBpiol S0002 B17"
/tissue_type="Tistil"
/dev_stage="1 DPA"
/lab_host="DH10B"
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Invergowrie, Dundee, DD2 5DA, Scotland, UX
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Fax: 00 44 1382 562426
Fax: 00 44 1382 562426
Fax: 01 41 1382 562426
Fax: 02 41 1382 182426
Seq primer: M13 reverse
Location/Qualifiers
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                                                                                                                                                                                                                                             EST 14-FEB-1997
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EBpi01 SQ002_B17_R pistil, 1 DPA, no treatment, cv Optic, EBpi01
Hordeum vulgare subsp. vulgare cDNA clone EBpi01_SQ002_B17 5', mRNA
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/note="Vector: Lambda ZAP II, The FB library (catalog #937201, Stratagene) was constructed by directional clouding and oligo d(T)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases 1 to 473)
Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A.,
Stevens, T.J., Robinson, M., Orpena, A.K., and Sikela, J.M.
Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Contact: Sikela JM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 B. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 30327070997
                                                                                                                                                                                                                                             mRNA
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/mol_type="mRNA"
/db_xref="ARCO (inhost):86662"
/db_xref="GDB:D082785E"
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                                                                                                                                                                                                                                      473 bp
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Location/Qualifiers
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us-09-604-231-1.rst

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Triticum aestivum (bread wheat)

Triticum aestivum

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Triticum.

I (bases 1 to 869)

S. Allaad,F. (crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,

Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,

Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,

Penniket,C., Roach,J.L. and Sarhan,F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops

Contact: Wm L Crosby
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1 (bases 1 to 785)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 785;
                                                                                              nessing, v. Sequencing of the maize endosperm ESTs Unpublished (2002) Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-3801 Eax: 732-445-3735 Email: jlai@waksman.rutgers.edu Seq primer: T3.
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iive 0; Mismatches
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Matches 138; Conservative
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                                                                                                                                                        Total Dasser 1 to 791)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USP
Sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:54126"
/dlone lib=Mxxed stage fosmid library of
var. California"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pristionchus pacificus"
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/strain="California"
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Similarity 46.9%; Pred. No. 0.23;
42; Conservative 0; Mismatches 161;
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Gaps

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EST 05-DEC-2003

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Bioinformatics
University of Saskatchewan, Department of Computer Science
10.101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [128,636].
Plate: Talt537 row: N column: 23.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        1. .869
/organism="Triticum aestivum"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="Wheat line PI 178383"
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/clone_Crgan: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart cDNA (Clontech)priming and non-directional cloning"
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Search completed: October 30, 2004, 17:04:56 Job time: 4442 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 29, 2004, 22:57:53 ; Search time 197 Seconds (without alignments) 1366.880 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-604-231-2 2363 1 MAMVFPSLVNGYDVAATMAA.....IEAGANLLNVAKKEAVPATP 468

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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NCBI_TaxID=1590;
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and vitamins.",
J. Biotechnol. 104:5-25(2003).

EMBL: EX927155; CAF21304.1; -.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                  Length 661;
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02-WAR-2004 (TrewBlrel. 27, Last sequence update)
02-WAR-2004 (TrewBlrel. 27, Last annotation update)
ENZYME II SUCROSE PROTEIN (BC 2.7.1.69).
                                                                                                                                                100.0%; Score 2363; DB 2;
100.0%; Pred. No. 3.6e-144;
iive 0; Mismatches 0;
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626;
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TIGRRAMS; TIGRO0830; PTBA; 1.
TIGRPAMS; TIGRO1996; PTS-III-BC-sucr; 1.
PROSITE; PS01035; PTS BIIB CYS; 1.
Complete proteome; Transferase.
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T'Complete genome sequence of Lactobacillus plantarum WCFS1.";
Theor. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
R HSSP: P20166; 1GPR.
R GO; GO:00166; 1GPR.
GO; GO:0016029; C:membrane; IBA.
GO; GO:0016029; F:protein-N(PI)-phosphohistidine-sugar phosph. . .,
R GO; GO:0016740; F:transport; IEA.
GO; GO:0016740; F:transport; IEA.
R GO; GO:0016740; F:transport; IEA.
R GO; GO:0016740; P:transport; IEA.
R GO; GO:0016910; P:transport; IEA.
R GO; GO:0010940; P:transport; IEA.
R InterPro; IPR011055; DUP,hybrid motif.
R InterPro; IPR001956; Ptrans_EIIE.
R InterPro; IPR001352; Ptrans_EIIE.
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STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Klerebezem M., Boekhorst W., Peters S.A., Sandbrink H.M.,
Fiers M.W.E.J., Stiekem W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing
De Vos W.M., Siezen R.J.;
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  Length
                                                Indels
; Score 2363; DB 2;
; Pred. No. 3.6e-144;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
sucrose PTS, EIIBCA (EC 2.7.1.69).
Name-ptsiECA, OrderedLocusNames=lp_0185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           651 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
       100.0%;
                                Best Local Similarity 100.
Matches 468; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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68454 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane
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510
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562
                                                        the sugar.
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MOD_RES
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                          313
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                                                                                                                                                                                                                                                         VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                                                                                                                                                          314 LYSAIVITGEHQTFPAIETQILANVAKTGGSFIFPVASMANIGQGAATLAIFFATKSQKQ 373
                                                                                                                                                                                                    253
                                                                                                                                                                                                                                                                                                                                                              486
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                                                                                                                                                                                                                                                                                                                                                                                                                                           596
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                                                                                                                                                                             1 MAMVFPSLVNGYDVAATWAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                         194 MINVLPSLVNGYSVATTMAAGKOVVWNVFGLHVAQAGYQGQVLPVLAVAYILATLEKFFH
                                                                                                                                                                                                                   KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                                                                                                                                                                                              Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
                                                                                                                                                                                                                                                                                                KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                                                                                                     237 LGVVSIDAPDNVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE
                                                                                                                                                                                                                                                                                                                                                                            297 AEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pediococcus pentosaceus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Pediococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 34, Last annotation update)
PTS system, sucross-specific IIABC component (BIIABC-Scr) (Sucross-permease IIABC component) (Phosphotransferase enzyme II, ABC component) (EC 2.7.1.69) (EII-Scr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAIKAAGYEVITPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEA--VPAT 467
                                                                                                                                        45.0%; Score 1062.5; DB 2; Length 651; 46.7%; Pred. No. 2.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PPE1.0;
Leenhouts K.K.J., Bolhuis A.A., Kok J.J., Venema G.G.,
"The sucrose and raffinose operons of Pediococcus pentosaceus
                                                                                                                                                           80; Mismatches 149; Indels
                                                                                                                     68514 MW; CBFB535EDDB73DD6 CRC64;
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR010973; PTS_II BC_
Pfam; PF00358; PTS_EIIA_I; I.
Pfam; PF00378; PTS_EIIB, I.
Pfam; PF00378; PTS_EIIB, I.
ProDom; PD001476; Ptrans_EIIB; I.
TIGRRAMS; TIGR00830; PTBA; I.
PROSITE; PS00371; PTS_EIIA, I.
PROSITE; PS00371; PTS_EIIA, I.
PROSITE; PS00371; PTS_EIIA, I.
PROSITE; PS01035; PTS_EIIB_C'S; I.
COMplete proteome; Transferase.
SEQUENCE 651 AA; 68514 MW; CBFBB335EDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                          221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTSA PEDPE
P43470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=scrA;
                                                                                                                                                                                                                                                                                                                    374
                                                                                                                                        Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373
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sugar phosphotransferase system (PTS), a major carbohydrate active—transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phosphoryler); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 LYSAIVITGLHQTFPAIETQLLANVAKTGGSFIFPVASMANIGQGAATLAIFFATKSQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.8%; Score 1058.5; DB 1; Length 651;
46.7%; Pred. No. 4.9e-60;
iive 78; Mismatches 151; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphocysteine (By similarity).
Phosphohistidine (By similarity)
Phosphohistidine (By similarity)
C87BA09D550A77F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00371; PTS EIIA 1; 1.
PROSITE; PS01035; PTS EIIB CYS; 1.
Phosphorylation; Phosphotransferase system; Sugar transport;
                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                       histidine + sugar phosphate.
-!- SUBCELIULAR LOCATION: Integral membrane
-!- SIMILARITY: COntains 1 PTS EIIB domain.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGR01995; PTG-II-ABC-beta; 1.
TIGREAMS; TIGR01996; PTS-II-BC-sucr; 1.
TIGREAMS; TIGR01992; PTS-IIBC-Tre; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z32711; CAA83668.1; --
EMBL; L32093; AAA25567.1; --
EMBL; L32093; AAA2567.1; --
HSSP; P20166; LGRA
InterPro; IPR011055; Dup hybrid motif.
InterPro; IPR001995; Ptrans EIIE.
InterPro; IPR001995; Ptrans EIIE.
InterPro; IPR001995; PTS EIIA.
InterPro; IPR010973; PTS EIIA.
Pfam; PF00358; PTS EIIA 1; I.
Pfam; PF00358; PTS EIIA 1; I.
ProDom; PD002243; PTS EIIA; I.
ProDom; PD001249; PTS EIIA; I.
ProDom; PD00146; PTS EIIB; I.
IGRRFAMS; TIGR00826; EIIB 91c; I.
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297 A--EAPA----EFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVS 349
                                                                                                                                                                                                                                                                                      PVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNINGTHFNPLKKQGDEVKAGE 409
                                             261 KSLTTSAGISAMLGITEPALFGVNLKLKFPFFIGLIASGISSFIIGLHVLSVSMGPAGI 320
                                                                                                                             237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE 296
                                                                                                                                                                                          --TTEEE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV-AKKE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=99173919; PubMed=10074089;
Luesink E.J., Marugg J.D., Kuipers O.P., De Vos W.M.;
"Characterization of the divergent sacBK and sacAR operons, involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unintercenteartor of the Autorigan eachs and sector involved in success dislication of the Autorigan eachs and sector of in success dislication by Lactococcus lactis.";

1. Bacteriol. 181:1924-1926(1999).

12. Bacteriol. 181:1924-1926(1999).

13. Bacteriol. 181:1924-1926(1999).

14. EMBL; 297015; CAB09690.1; -..

15. GO; GO:0016020; C:membrane; IEA.

15. GO; GO:0016932; P:protein-N(PI)-phosphohistidine-sugar phospho...;

15. GO; GO:0016940; P:protein-N(PI)-phosphohistidine-sugar phospho...;

15. GO; GO:0016940; P:protein-N(PI)-phosphohistidine-sugar phospho...;

15. GO; GO:0016940; P:prosphoenolpyruvate-dependent sugar phospho...;

15. GO; GO:0016940; P:prosphoenolpyruvate-dependent sugar phospho...;

16. GO; GO:0016940; P:prosphoenolpyruvate-dependent sugar phospho...;

16. GO; GO:0016940; P:prosphoenolpyruvate-dependent sugar phospho...;

17. Roje GO; GO:0010532; P:rans EIIB.

18. InterPro; IPR00137; PTS_EIIA.

19. Riam; PP00358; PTS_EIIA.

19. Pfam; PP00358; PTS_EIIB.

10. Roje GO; GO:0016973; PTS_EIIB.

10. Roje GO; GO:0016973; PTS_EIIB.

10. Roje GO; GO:0016973; PTS_EIIB.

11. Roje GO; GO:0016973; PTS_EIIB.

12. Roje GO; GO:0016973; PTS_EIIB.

13. Roje GO; GO:0016973; PTS_EIIB.

14. Roje GO; GO:0016973; PTS_EIIB.

15. Roje GO; GO:0016973; PTS_EIIB.

16. Roje GO; GO:0016973; PTS_EIIB.

17. Roje GO; GO:0016973; PTS_EIIB.

18. Roje GO; GO:0016973; PTS_EIIB.

19. Roje GO; GO:0016973; PTS_EIIB.

10. Roje GO; GO:0016973; PTS_EIIB.

10. Roje GO; GO:0016973; PTS_EIIB.

10. Roje GO; GO:0016973; PTS_EIIB.

11. Roje GO; GO:0016973; PTS_EIIB.

12. Roje GO; GO:0016973; PTS_EIIB.

13. Roje GO; GO:0016973; PTS_EIIB.

14. Roje GO; GO:0016973; PTS_EIIB.

15. Roje GO; GO:0016973; PTS_EIIP.

16. Roje GO; GO:0016973; PTS_EIIP.

17. Roje GO; GO:0016973; PTS_EIIP.

18. Roje GO; GO:0016973; PTS_EIIP.

19. Roje GO; GO:0016973; PTS_EIIP.

10. Roje GO; GO:0016973; PTS_EIIP.

10. Roje GO; GO:0016973; PTS_EIIP.

10. Roje GO; GO:0016973; PTS_EIIP.

10. Roje GO; GO:0016973; PTS_EIIP.

10. Roje GO; GO:0016973; PTS_EIIP.

10. Roje GO; GO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Enzyme II sucrose protein (EC 2.7.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 40.7%; Score 962; DB 2; al Similarity 42.9%; Pred. No. 8.2e-54; 203; Conservative 89; Mismatches 145
                                                                                                                                                                        : | :: | : | : | :: | | | | | :: | IGPIAIAPKSIPSFMMGAIISFVIAFVGTYLYGKKAMK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probon; PD001476; Ptrans_EIIB; 1.
Probon; PD00243; PTS EITA; 1.
TIGRFAMS; TIGR00830; PTBB; 1.
TIGRFAMS; TIGR01996; PTS-II-BC-sucr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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PROSITE; PS01035; PTS_EIIB_CYS;
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                                                                                     AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV 356
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MEDIJINE=21822499; PubMed=11832506;
Dudez A.M., Chaillou S., Hissler L., Zagorec M.;
Champonier-Verges M.C., Alpert C.A., Zagorec M.;
Pphysical and genetic map of the Lactobacillus sakei 23K chromosome.";
Microbiology 148:421-431(2002).
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                                                                                                                          VAPPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R GO; GO:0016620; C:membrane; IEA.

R GO; GO:0016620; C:membrane; IEA.

R GO; GO:0008982; F:protein-N(PI)-phosphohistidine-sugar phosph. . .;

R GO; GO:0008351; F:sugar porter activity; IEA.

R GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. . .;

R GO; GO:000810; P:transport; IEA.

R InterPro; IPR01125; Dup hybrid motif.

R InterPro; IPR01127; PTS EIIA.

R Pfam; PP03378; PTS EIIA.

R Probom; PD002243; PTS EIIA.

R Probom; PD002243; PTS EIIA; 1.

R Probom; PD002243; PTS EIIA; 1.

R PROSITE; PS00371; PTS EIIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                       649
                                                                                                                                                                                                                                                                                                                                467
                                                                                                                                                                                                                                                                                                                                                               417 DAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL--LNVAKKEAVPAT
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44.2%; Pred. No. 7.3e-55;
rive 90; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dudez A.-M., Chaillou S., Zagorec M.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401046; AAK92528.1; -..
HSSP; P45618; 2GPR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sucrose-epecific enzyme II of the PTS (Fragment).
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Best Local Similarity
Matches 211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactobacillus sakei
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SEQUENCE
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FUNCTION: This is a component of the phosphoenolpyruvate-dependent
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331
585
664 AA;
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                                                             the sugar.
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MOD RES
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     KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                121 VYSPIVITGIHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSB 174
                                                                                   175 KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
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                                                                                                                                                                   295 AEAEAPAEFSNDSTIIQ-----APLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ 346
                                                                                                                                                                                                          LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNINGTHFNPLKKQGDEVK 406
                                                               314 PYSAIVVTGLHQSFPALETMLITNYQHSGIGGDFIFPVAACANMAQAGATFALLFVTKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=89123027; PubMed=2536656; Sato Y., Poy F., Jacobson G.R., Kuramitsu H.K.; all Poy F., Jacobson G.R., Kuramitsu H.K.; "Characterization and sequence analysis of the scrA gene encoding enzyme IIScr of the Streptococcus mutans phosphoenolpyruvate-dependent
                                                                                             GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK
                                                                                                                                                                                                                                                                                                                                          "Genome sequence of Streptococcus mutans UA159, a cariogenic dental pathogen.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K.;
"Isolation, characterization and sequence analysis of the scrK gene
encoding fructokinase of Streptococcus mutans.";
J. Gen. Microbiol. 139:921-927(1993).
                                                                                                                                                                                                                                                   AGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-UALIS9 / ATCC 700610 / Serotype c;

MEDLINE-22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;

Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.

Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,

Perretti J.J.;
                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
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                                                                                                                                                                                                                                                                                                                           664
                                                                                                                                                                                                                                                                                                                                                                                             Component) (EC 2.7.1.69) (EII-SGr).
Name=scrA; OrderedLocusNames=SMU.1841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sucrose phosphotransferase system.";
J. Bacteriol. 171:263-271(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 639-664 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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sugar phosphotransferase system (PTS), a major carbohydrate active—transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the principle phosphorylation site (the donor is phosphoryler); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMVFPSLVNGYDVAATMAAGEMP-----MWSLFGLDVAQAGYQGTVLPVLVVSWILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00371; PTS BILA 1; 1.
PROSITE; PS01035; PTS_BILB_CYS; 1.
Complete proteome; Phosphorylation; Phosphotransferase system; Sugar transport; Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphocysteine (By similarity).
Phosphohistidine (By similarity)
Phosphohistidine (By similarity)
809B63B32281A9A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                        DB 1;
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EMBL, AE015011, AAN59464.1; -
EMBL, D13175, BAA02466.1; -
EMR, D13175, BAA02466.1; -
EMR, B32243, B32243.
HSSP, B08837, 1GGR.
InterPro; IPR011055; Dup_hybrid_motif.
InterPro; IPR011055; Ptrans EIIB.
InterPro; IPR001352; Ptrans EIIC.
InterPro; IPR00127; PTS EIIA.
InterPro; IPR010973; PTS EIIA.
Pfam; PF00358; PTS EIIA.
Pfam; PF00358; PTS EIIB.
Pfam; PF00378; PTS EIIB.
Pfam; PF00378; PTS EIIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD002243; FTS EIIA; 1.
Probom; PD0012476; PTS EIIA; 1.
TIGRFAMS; TIGR00826; EIIB glc; 1.
TIGRFAMS; TIGR019830; PTBA; 1.
TIGRFAMS; TIGR01995; PTS-II-ABC-beta; 1.
TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
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---GGAGKYWDIFGLHVSQTNYQYQVIPVLVAVWLLAFLEKRFH
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                                                                                                                                                                                                                                                               PRELIMINARY;
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   194 MIMITPAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               sucrose specific.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=33959;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NCC 533;
PubMed=14966310;
                                                                                                                                                                                                                                                                AAS09702
AAS09702;
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                                                                                                        QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY-GLGEIEAGANLLNVA 459
                     ||:||:||||| :|| | : ::|| :::| | | AVSLGSAGFLGFLSIKASIPFYVTYGYG----KTKAVDVFAAEAA 488
                                                                         VPIKGOLVSPVSGKIVVAFPSGHAFAVRIKAEDGSNVDILMHIGFDIVNLNGTHFNPLKK 400
                                                                                                                604 ADQKIKKGDVLGTFDSDKIAEAGLDNTTMFIVTNTADYASVETLASSGTVAVGDSLLEVK 663
           AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP 287
                                                                                                                                                                                                                                                                                                                     489 VEEAIEEVQ-EIPEEAASAANKAQVTDEVLAAPLAGEAVELTSVNDFVFSSEAMGKGIAI
                                                                                  ---IIQAPLTGEAIALSSVSDAMFASGKLGSGVAI
                                                                                                                                                                                                                                   system EllABC,
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                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
phosphoenolpyruvate-dependent sugar phosphotransferase
sucrose specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95FA74C533CE9541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.7%; Score 914.5; DB 2;
llarity 41.3%; Pred. No. 9.5e-51;
Conservative 88; Mismatches 160;
                                                                                                                                                                                              647 AA
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SEQUENCE 647 AA; 69202 MW; 95FA74C53
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                            VPAGTTKAEAEAPAEFSNDST---
                                                                                                                                                                                                                                                    OrderedLocusNames=LJ0519;
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                               Lactobacillus johnsonii
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=33959;
                                                                                                                                                                                                                                                                                                           STRAIN=NCC 533;
PubMed=14966310;
                                                                                                                                                        K 664
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1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VYSPIVITGLHOSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE 174
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                                                                                                                                                                                                                                                   KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                         VYSPIVITGLHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE 174
                                                                                                                                                                                                                   KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                       290 AGTIKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVS
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIABC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R., Mollet B., Mercenler A., Klaenhammer T., Arigoni F., Schell M.A.; Mollet B., Mercenler A., Klaenhammer T., Arigoni F., Schell M.A.; Lactobacillus johnsonii NCC 533.", Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

BMBL; AE017206; AAS09702.1; -.

Pyruvate; Transferase.

SEQUENCE 647 AA, 69202 MW, 95FA74C533CB9541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 LLCEFDIDAIKAAGYEVITPIVVSNYKKIGPVNTYGLGEIEAGANLLNVAKK 461
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Throctological and comparative genomic analyses of an operon involved in fructooligosaccharide utilization by Lactobacillus acidophilus.";

Tructooligosaccharide utilization by Lactobacillus acidophilus.";

Enc. Natl. Acad. Sci. U.S.A. 100.8957-8962(2003).

REMEL, AY177419; AA038866.1;

RGO; GO:001620; C:membrane; IEA.

RGO; GO:001620; C:membrane; IEA.

RGO; GO:0016392; F:protein-N(P)-phosphohistidine-sugar phosph. .; IEA.

RGO; GO:0016740; F:transferase activity; IEA.

RGO; GO:0016740; F:transferase activity; IEA.

RGO; GO:0016740; F:transferase activity; IEA.

RGO; GO:000591; P:prosphoenolypurvate-dependent sugar phospho. .; IEA.

RGO; GO:0009401; P:prosphoenolypurvate-dependent sugar phospho. .; IEA.

RINEEPPC; IPRO0135; P:Tans EIIB.

RINEEPPC; IPRO0135; PTS_EIIA.

RINEEPPC; IPRO1373; PTS_EIIA.

REAM; PPO0358; PTS_EIIB; I.

REAM; PPO0358; PTS_EIIB; I.

REAM; PRO1378; PTS_EIIE; I.

REAM; PRO1378; PTS_EIIE; I.

REAM; PRO1378; PTS_EIIE; I.
SYSAIVTTGLHQSFPAVETQLLAEYARGRGSGDFIFVTACMANVAQGAATFAIYFLTKNE 362
                                                                   422
                                                                                                                                                                                                                  350 PVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGE 409
                                                                                                                                                                                                                                                       595
                              KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
                                              235 GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAALAYGLY----LVRRNGSIDPDATAAPVP
                                                                                                                                                    290 AGTTKAEARAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVALVPTKGQLVS
                                                                                                                                                                         410 LLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                                                                                   38.1%; Score 901; DB 2; Length 649; 40.8%; Pred. No. 7.1e-50; live 81; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes, Lactobacillales; Lactobacillaceae;
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Last annotation update)
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ProDom; PD002243; PTS EITA; 1.
TIGRFAMS; TIGR00830; PTBA; 1.
TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequ
01-MAR.2004 (TrEMBLrel. 26, Last anno
Sucrose PTS transporter (EC 2.7.1.69)
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillus acidophilus,
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Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1579;
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PubMed=12847288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactobacillus
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1 MAMVEPSLVNGYDVAATWAAGEMPWWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60

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61 KRLKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                              121 VYSPIVITGLHQSFPPIELELF-----NQGGSFIFATASMANIAQGAACLAVFFLAKS 173
                                                                                                                                             303 SYSAIVITGIHQSFPAVETQILAAFAKNPASSGDFIFVTACMANVAQGAATFAVYFLTKN 362
                                                                                                                                                                                                                                                                                                                                                                      292 -----TTKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKG 345
-----GGATKFWDIFGLHVAQTNYQYQVIPVLVAVWVLSIFEKYFH 242
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                                                                                                                                                                                                                                                                                                              346 QLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEV 405
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SEQUENCE FROM N.A.
STRAIN-V583 / ATCC 700802;
WEDLINE-22550857; PubMed-12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.B., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinksc L.M., Beanan M.J.,
Daugherty S.C., Davey R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
Fraser C.M.;
                                                                                                                                                                                                   174 EKLKGLAGASGVSAVLGITEPAIFGVNIRLRWPFFIGIGTAAIGGALIALFNIKAVALGA
                                                                                                                                                                                                                                                                                    AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAG--
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R QO; GO:0016020; C:membrane; IEA.

R QO; GO:0016020; C:membrane; IEA.

R QO; GO:0005821; F:protein-N(FI)-phosphohistidine-sugar phosph. . .;

R QO; GO:0005321; F:sugar porter activity; IEA.

R QO; GO:0005810; P:phosphoenolpyruvate-dependent sugar phospho. . .;

R GO; GO:0006810; P:phosphoenolpyruvate-dependent sugar phospho. . .;

R InterPro; IPR010155; Dup hybrid motif.

R InterPro; IPR001352; Ptrans EIIE.

R InterPro; IPR001375; PTS EIIA.

R InterPro; IPR00137; PTS EIIA.

R InterPro; IPR00137; PTS EIIA.

R Pfam; PF00358; PTS EIIB.

R Pfam; PF00358; PTS EIIB.

R Pfam; PF00357; PTS_EIIB.

R Pfam; PF00357; PTS_EIIB.

R Pfam; PF00357; PTS_EIIB.
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Science 299-2071-2074(2003).
EMBL; AE016833; AAO83060.1; -.
HSSP; P20166; IGPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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01-JUN-2003
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DOI=10.1128/JB.183.16.4823-4838.2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYSPIVITGLHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK 294
                                                                                                                                                                                                                                                                                                                                      481 INTNQIANADEPITVETIVSPLAGEITTLGSVNDFVFSSESIGKGIAIXPNGNTIYSPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIVOVVFETGHAYDLKS----NTGAEILIHVGIDTVSLNGKGFT--KKVGAKQKVKKGEV
                                                                                                                                                                                                                                                                                                           MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                                                                                                                                                                                                            KRLKGTADFLITPVLTLLITGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 AEAEAPAEFSNDSTI--IQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG--DEVKAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIBAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGTFDSTVÍTNSGLDDŤÍMVIVÍTNSKDYSEVIPITKNIVTEGALÍTI 642
                                                                                                                                                                                                                       643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transport and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2004 (TrEMBLrel. 28, Last annotation update)
01-007-2004 (TrEMBLrel. 28, Last annotation update)
SGTA (Fusion: PTS system, beta-glucosides specific IIABC
                                                                                                                                                                                                                       DB 2; Length
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                               68532 MW; 752F65D8154AA06C CRC64;
                                                                                                                                                                                                                     35.2%; Score 832.5; DB 2; 39.3%; Pred. No. 1.8e-45; iive 84; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 824;
MEDLINE=20391269; PubMed=10937490;
Tangney M., Mitchell W.J.;
Tangney M., Mitchell W.J.;
in Clostridium acetabolic operon for sucrose in Clostridium acetabutylicum ATCC 824.";
J. Mol. Microbiol. Biotechnol. 2:71-80(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 AA
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
      Pfam, PF02378; PTS_EIIC; 1.
ProDom; PD001476; Ptrans EIIB; 1.
ProDom; PD001243; PTS_EIIA; 1.
TIGRFAMS; TIGR00830; PTBA; 1.
TIGRFAMS; TIGR01996; PTS_II-BC-sucr; 1.
PROSITE; PS010371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIA_CYS; 1.
Complete Protecome; Plasmid.
SEQUENCE 643 AA; 68532 MW; 752F65D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=scrA; OrderedLocusNames=CAC0423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                    Matches 184; Conservative
                                                                                                                                                                                                                                                Similarity
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360 PSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAI 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 VSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 AIVKQGSFLNYIIAMI----LAFGGAFIIAMVLGIKBEITEEDLNKETVNKDIKVEEVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKGTADFLITPVLTLLITGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 SLIVITGIHHSFHAIBAGLLANPAIHKNFLLPIWSMANVAQGGAALAVYFKTRDKKMKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AAPASFSCLLGITEPAIFGVNLRYTKPFIAGALGGAIGGGYIVFTKVAMTAVGVTGIPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 MVFPSLVNGYDVAATMAAGEMPMMSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Noelling J., Breton C., Onelchenko M.V., Makarova K.S., Zeng Q., Noelling J., Breton W., Onelchenko M.V., Makarova K.S., Zeng Q., Tatusov R., Lee H.M., Dubons J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; Gencer G.N., Koonin E.V., Smith D.R.; Gencer and comparative analysis of the solvent-producing bacterind. Clostridium acetobutylicum."; J. Bacteriol. 183:4823-4838(2001).

Bacteriol. 183:4823-4838(2001).

BRML; ARO07557; AAK78403.1; -.
PIR; H96951; H96951.
                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 AA; 67596 MW; B835AB0238FCA436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 759.5; DB 2; 36.7%; Pred. No. 9.2e-41; iive 80; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00371; PTS EIIA 1; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|:|: | ||:
| KEKAVSPIVLTIVTNHEDMGFVNS 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 627 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528
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              295 AEAE---APAEFS-NDSTIIQAPLIGEAIALSSVSDAMFASGKIGSGVAIVPTKGQLVSP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stabhylococcus xylosus.";
Mol. Gen. Genet. 241:33-41(1993).
-!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active -transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPP); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
                                           351 VSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDBVKAGEL
                                                                                                                                        BC component)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphate.
histidine + Sugar phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the sucrose-
                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
PTS system, sucrose-specific IIBC component (BIIBC-Scr) (Sucrose-permase IIBC component) (Phosphotransferase enzyme II, BC component)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, S39978; S39978.

R InterPro; IPR001996; Ptrans_EIIB.

R InterPro; IPR001952; Ptrans_EIIB.

R InterPro; IPR010973; PTS_II_BC_sucr.

R fam; PF00367; PTS_EIIB; 1.

R ProDom; PD001476; PTS_EIIB; 1.

R PTGRFAMS; TIGR00395; EIIB, glc; 1.

R TIGRFAMS; TIGR01995; PTS-III-BC-beta; 1.

R TIGRFAMS; TIGR01995; PTS-III-BC-sucr; 1.

R TIGRFAMS; TIGR01992; PTS-III-C-re; 1.

R TIGRFAMS; TIGR01992; PTS-III-C-re; 1.

R TIGRFAMS; TIGR01992; PTS-III-C-re; 1.

R TIGRFAMS; TIGR01992; PTS-III-C-re; 1.

R TIGRFAMS; TIGR01992; PTS-III-C-re; 1.

R SOGITE; PS01035; PTS EIIB, CYS; 1.

N Inner membrane; Phosphorylation; Phosphotransferase system; Sugar transport; Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DSM 20267 / Isolate C2A;
MEDLINE=94049666; PubMed=8232009;
Wagner B., Goetz F., Bruckner R.;
"Cloning and Characterization of the scrA gene encoding t
specific Enzyme II of the phosphotransferase system from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                          480 AA
                                                                                                                                                                                                     411 LCEFDIDAIKAAGYEVTTPIVVSN 434
                                                                                                                                                                                                                                                     577 LVTFDIAAIKEAGYPVVTPIVVTN 600
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X69800; CAA49461.1; -.
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EC 2.7.1.69) (EII-Scr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus xylosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYSPIVITGLHQSFPPIELELFNQGGSF1FATASMANIAQGAACLAVFFLAKSEKLKGLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .; IEA.
                                                                                                                                                                                                                                                                              STRAIN=V583 / ATCC 700802,
MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Baneriel L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.
Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.U., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
                                                                                                                                                              Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK
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R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016020; E:protein-N(PI) -phosphohistidine-sugar phosph. ..;
R GO; GO:0008401; F:protein-N(PI) -phosphohistidine-sugar phosph. ..;
R GO; GO:000401; P:phosphoenolpyruvate-dependent sugar phospho. ..;
R GO; GO:0006810; P:transport; IEA.
InterPro; IPR0011055; Purans EIIB.
R InterPro; IPR001125; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
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InterPro; IPR001127; PTS EIIA.
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InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
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InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
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InterPro; IPR001127; PTS EIIA.
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InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
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InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
InterPro; IPR001127; PTS EIIA.
Inter
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                                                            01-MAR-2004 (TrEMBLrel. 24, Last sequence update)
PTS system, beta-glucoside-specific IIABC component
Enterconcurs face.
       626 AA.
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ProDom; PD002243; PTS EIIA; 1.
TIGRFAMS; TIGR00830; PTSA; 1.
TIGRFAMS; TIGR01895; PTS-II-ABG-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00371; PTS_EIIA_1; UNKNOMN_1.
PROSITE; PS01035; PTS_EIIB_CXS; 1.
                                           (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis.";
Science 299.2071-2074(2003).
EMBL; AE016955; AAO82308.1; --
HSSP; P08837; 1GGR.
  PRELIMINARY;
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                              01-JUN-2003
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                        Q831B4;
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Job time : 201 secs
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                                   SEQUENCE
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The complete genome sequence of the alkaliphilic bacterium Bacillus
The complete genome sequence comparison with Bacillus subtilis.";
The complete genome sequence comparison with Bacillus subtilis.";
The complete genome sequence comparison with Bacillus subtilis.";
The complete genome sequence comparison with Bacillus subtilis.";
The complete genome sequence comparison with Bacillus subtilis.";
The complete genome sequence comparison with Bacillus subtilis.";
The complete genome sequence comparison with Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
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                                                                                                                                                       Gaps
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
PTS system, beta-glucoside-specific enzyme II, ABC component.
                                                           (By similarity)
     BIIB.
EIIC.
Phosphocysteine (By similarity)
                                                                                                                  DB 1; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Me
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 GFLGVVSIDAPD--MVMFLVCAVVTFFIAFGAAIAYGLYLVRRN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIPGFISISGONNGWLHYGIAMIIAFIVAFGVTYALSYRKKYRN 477
                                                                                                                                                     81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacceria, Firmicutes, Bacillales, Bacillaceae, Bacillus NCBI_TaxID=86665;
                                                           Phosphohistidine (By simi AB4E1D9785D84E47 CRC64;
                                                                                                                  / Match 29.7%; Score 701; DB 1; Local Similarity 51.4%; Pred. No. 4.1e-37; les 146; Conservative 49; Mismatches 81;
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     7 BI
480 EI
26 Ph
325 Ph
51326 MW;
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Q9KG19;
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                                                                                                                                                                  122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SI---DAPDMVMFLVCAVVTFFIAFGAALAYGLYLVRRNGSIDPDATAAPVPAGTTKAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 IFYPEDGRGFVAFVIAILISFVLA----AVLTYIVGFKDPVDDEDTLSNESGSENEVKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 AFPSGHAFAVRIKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID
                                                                                                                                       2 AMVFPŞLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK
                                                                                                                                                                                                                                      237 KIHEAVKNIVTPLILLVVIVPVTLILLGPIGVXLGNGIASVIQELFTFSPVLAGAIVAGI
                                                                                                        21;
                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                  6F0218011686ADD5 CRC64;
                                                                   Query Match
29.4%; Score 695.5; DB 2;
Best Local Similarity 32.8%; Pred. No. 1.2e-36;
Matches 152; Conservative 108; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: October 29, 2004, 23:14:21
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
SEQUENCE 630 AA; 66978 WW; 6F0
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

Run on:

October 29, 2004, 23:05:49 ; Search time 40 Seconds (without alignments) 1125.736 Million cell updates/sec

US-09-604-231-2 2363 1 MAMVFPSLVNGYDVAATMAA.....IEAGANLLNVAKKBAVPATP Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		phosphotransierase	trans	fusion, PTS system	scrA protein - Sta	PTS system, beta-q	Ω	PTS system, beta-q	system,	sphotrans	trehalose PTS syst		System TIABO	sphotransferas	PTS System, Sucros	svstem.	sphotrans	beta-qlucoside per		- 54	യ	beta-glucoside-spe	PTS system, beta-o	thetical		hypothetical prote	7	Ψ.		sphotransferas
SU D	044567	Λ.	н .	H96951	839978	H83686	AB1167	AC1436	$^{\circ}$	868599	C95220	AD1078	F95200	E98067	F82432	D90038	A99084	I40406	JQ0781	T47097	B42603	AC1421	D97073	D86807	AC1204	A97935	B95067	C69725	8392	2597
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Length	651	1 5	9 0	179	480	630	617	633	636	632	655	634	627	627	479	480	705	609	479	609	631	617	628	636	618	612	612	470	470	625
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beta-qlucoside-spe	hypothetical profe	phosphotransferase	PTS SVRTEM SILVEDS	phosphotransferase	sac operon requiat	PTS SVSTEM trebalo	Jevanslichase synth	PTS SYSTEM trebalo	nhosphotransferase	trehalose specific	phosphotransferase	protein-Nni-nhosnh	PPS system engage	hypothetical prote	PTS enzyme II, ABC
AB1423	C89813	862331	H83881	WOEBST	139868	AG1231	JU0293	AF1585	A39938	A98281	C65236	AI0449	A86122	A89781	B96970
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640	475	456	458	455	372	494	459	494	460	473	473	483	473	681	665
21.5	21.0	20.7	20.6	20.0	19.8	17.3	17.2	16.8	16.5	15.5	15.5	15.5	15.2	14.7	14.6
509	496	489	487	473	467	408	406	396.5	390	367	367	367	360	348.5	345
30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	844257	phosphotransferase system enzyme II (EC 2.7.1.69), sucrose specific - pediococcus pentoss	C;Species: Pediococcus pentosaceus	C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text change 09-Jul-2004	C;Accession: S44257	R; Leenhouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema. G.G.	submitted to the EMBL Data Library, April 1994	A; Description: The sucrose and raffinose operons of Pediococcus neutosarens ppg1 0	A; Reference number: S44252	A; Accession: S44257	A; Molecule type: DNA	A;Residues: 1-651 <lee></lee>	A; Cross-references: UNIPROT: P43470; EMBL: Z32771; NID: G493728; PIDN. CBa83668 1. DID. A47604	C, Genetics:	A;Gene: scrA	C;Superfamily: phosphotransferase system engame II sucresserancific. whoseholders
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phosphotransterase : C;Keywords: phosphotransferase
F;488-640/Domain: phosphotransferase system glucose-specific enzyme II, factor III homolc

5 Gaps 23; Query Match 44.8%; Score 1058.5; DB 2; Length 651; Best Local Similarity 46.7%; Pred. No. 1.3e-64; Matches 221; Conservative 78; Mismatches 151; Indels 23;

120 253 9 1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFGL 61 δ 엄 δ qq

 δ g

313

236 177 KGLAGASGVSAVLGITEPAIFGVNLRIRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF ઠે QQ

296 237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE ð 셤

AEAPAEFSNDSTIIQAPLTGEALALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV 356 297 487 à a

416 357 VAFPSGHAFAVRIKAEDGSNVDILMHIGFDIVNLNGTHFNPLKKQGDBVKAGELLCEFDI à d

g à

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A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: H96951
A; Status: preliminary
A; Mollecule 'type: DNA
A; Residues: 1-627 < KUR>
A; Residues: 1-627 < KUR>
A; Residues: 1-627 < KUR>
A; Experimental source: Clostridium acetobutylicum ATCC824
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C;Species: Staphylococcus xylosus
C;Species: 3-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 33978
R;Wagner, E.; Goetz, F.; Brueckner, R.
Nol. Gen. Genet. 241, 33-41, 1993
A,Title: Cloning and characterization of the scrA gene encoding the sucrose-specific enz A;Reference number: S39976; MUID:94049686; PMID:8232209
                                                                                                                                                                                                                             C.Genetics:
A.fdene. CACC0423
C.Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
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A;Cross-references: UNIPROT:P51184; EMBL:X69800; NID:g407905; PIDN:CAA49461.1;
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
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; Pred. No. 2.2e-40;
49; Mismatches 81; Indels
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                                                                                                                                                                                                                                                                                                                                                                  80; Mismatches 176;
                                                                                                                                                                                                                                                                                                                      Score 759.5; DB Pred. No. 3e-44;
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ilarity 36.7%;
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Best Local Similarity 51.4%;
Matches 146; Conservative 4
Bacteriol. 183, 4823-4838,
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Best Local Similarity
Matches 163; Conserv
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                                    DAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL--LNVAKKEAVPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.4%; Score 953.5; DB 1; Length llarity 42.6%; Pred. No. 1.9e-57; Conservative 89; Mismatches 156; Indels
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Matches 205; Conserv
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Cispecies: Madueno, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
Altile: Comparative genomics of Listeria species
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AB167
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A; Comparative genomics of Listeria monocytogenes
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;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase s
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Acceston: AC1436
F;Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
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185 ALVYPTMINLENEGAHITFLQIP------VVLMSYSFSVIPIILAVWFLSILBRFINS 236
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Best Local Similarity 34.8%; Pred. No. 7.4e-40;
Matches 154; Conservative 82; Mismatches 162; Indels
                                     630
                           588 RITAAGYDVITPVLITNAKQFSNVQTTDKREVTSEDLLIHVIK
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83686
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
                                                                                                                                                                                               LVYSPIVITGLHQSFPPIELELF----NQGSFIFATASMANIAQGAACLAVFFLAK-SE 174
MILVHPELMSAYDYPKALEAGKEIPHWNLFGLEINQVGYQGQVLPMLVATYILATIEKGL 253
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                                                             HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG
                                                                                                                                                                                                                                                                                                                              KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFLGVVSIDAPD--MVMFLVCAVVTFFIAFGAAIAYGLYLVRRN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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29.4%; Score 695.5; DB 2;
Best Local Similarity 32.8%; Pred. No. 7e-40;
Matches 152; Conservative 108; Mismatches 182;
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- Listeria

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Indels

Pred. No. 2.2e-38; Mismatches

34.0%; Fi

234 107 294

47

- GLDVAQAGYQGTVLPVLV

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TETXAHTSTGTGEKEE------ISSPFNGSVITLSBIXDEAFSSGALGEGTAIE 521
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                                                                                                                                                                                                                                                                                          VMLKIKQQKVKTLSVPAFISGIFGVTEPAIYGVTLPLKRPFIISCIAAAVGGAIIGLFRS
                                                                                                                                                                                                                                                                                                                                  227 KAVALGAAGFIGVVSI----DAPDMVMF-LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDP
                                                                                                                                                                                                                                                                                                                                                                415 QGYIIGGLGIFGIPSFLHPADGMDAGFWGIVIAVVVAFV-LGFILTYLFGLKSGNASDBQ
                                                                                                                                                               108 DFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLA
                                                                                                VSWILATIEKFLHKRLKGTADFLITPVLTLLIGFLTFIAIGPAMRWVGDVLAHGLQGLV
                                                                               AMVFPSLVNGYDVAATMAAGEMPMWSLF--
                                                   163; Conservative
                                  Local Similarity
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Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Malok, C.; Sciluteter, T.; Sinoes, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Restaus: preliminary
A; Molecule type: DNA
A; Residues: 1-633 <GIA>
A; Experimental source: strain Clip11262
C; Genetics:
C; Genetics:
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                                                                                                                                                                                                                                                 C, Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
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C83724
PTG system, beta-glucoside-specific enzyme II, ABC component bglP [imported] - Bacil:
C;Species: Bacillus halodurans
C;Jate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83724
C;Accession: C83724
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83724
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTKAEAERAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETNVTEGETLIE----RETIPAPVVGRIVTLADVKDEAFSSGALGKGVALIPTVGRVVA 526
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                                                                                                                                                                                                                                                                                                                                                                  EKFLHKRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGG
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                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                   Length 633;
                                                                                                                                                                                                                                                                                tch 28.5%; Score 674; DB 2; Length 63 al Similarity 36.2%; Pred. No. 2.1e-38; Indels 161; Conservative 75; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLCEFDIDAIKAAGYEVITPIVVSN 434
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GDEVKAGELLCEFDIDAIKAAGYEVITPIVVSNYKKTGPVNTYGLGEIBAGANLLNVAK 460

PTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQ

401

DATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIV

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281 473 341

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- Streptococcus sobr
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phosphotransferase system enzyme II (EC 2.7.1.69), sucrose-specific - Streptococco NyAlternate names: sucrose-specific enzyme II C;Species: Streptococcus sobrinus A;Variety: strain 6715 C;Aariety: strain 6715 C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999 C;Accession: S68599 R;Chen, Y.Y.W.; LeBlanc, D.J. Infect: Immun. 61, 2602-2610, 1993 A;Title: Sequence analysis of scrA and scrB from Streptococcus sobrinus 6715. A;Reference number: S68599 MUID:93273516; PMID:8500898 A;Accession: S68599 A;Status: preliminary A;Moslecule type: DNA A;Residues: 1-632 cHE> A;Cross-references: EMBL:L06791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: scrA
C;Superfamily: phosphotransferase system enzyme II sucrose-specific;
C;Keywords: phosphotransferase; sugar transport system
C;Keywords: phosphotransferase system glucose-specific enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
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Best Local Similarity 36.4%; Pred. No. 2.4e-38;
Matches 168; Conservative 76; Mismatches 197; Indels
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F.; Hira and PIDN:BAB04

A;Cross-references: UNIPROT:09KF90; GB:AP001509; GB:BA000004; NID:g10173176; A;Experimental source: strain C-125

1-636 <STO>

A; Molecule type: DNA A; Residues: 1-636 <S'

Genetics

A,Gene: bglP C,Superfamily: phosphotransferase system enzyme II sucrose-specific, \mathcal{C}, \mathcal{S} uperfamily:

Score 673.5; DB 2; Length 636;

28.5%;

Query Match

phosphotransferase

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<u>:</u> ::

239 Qy 338 VAIVPTKGQLVSPVSGKIVVAPPSGHAPAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP 397 L	RESULT 11 AD1076 PTS System, beta-glucosides specific enzyme IIABC homolog lmo0027 [importe C.Species: Listeria monocytogenes C.Species: Listeria monocytogenes C.Species: Listeria monocytogenes C.Species: Listeria monocytogenes C.Species: Listeria monocytogenes C.Species: Listeria monocytogenes C.Species: Listeria monocytogenes D.; Jones 24, 449-62; Lochaud, E.; Durand, A.; Dasurget, O.; Bartian, K. D.; Jones 24, 449-62; Lochaud, E.; Durand, A.; Dasurget, O.; Bartian, C.; Schluecer, T.; Since, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss A; Tier comparative genomics of Listeria species A; Tier: Comparative genomics of Listeria species A; Tier: Comparative genomics of Listeria species A; Residues: Preliminary A; Rolecule type: DNA A; Residues: Lo34 (GLA) A; Residues	DD 352 QY 235 QY 284 DD 479 QY 344 QY 404 DD 522
Db 306 LQQVIVVTGVHHIFNFLETQLLAETKANPFNPLLSAATAGQVGAVLAVAVKTKSAKLKAL 180 AGASGVSAVLGITEPAIFGVNLRIRNPFFIGIGTAAIGGALIALFNIKAVALGAAGTGGV Db 366 AYPSALSAALGITEPAIFGVNLRYGKPFVMGLVGGSAGGFIAALVGLKATGMSVTVLPGL 240 VSIDAPDNVMFLVCAVVTFFIAFGAAIAYGLYGVRRNGSIDPDATAAPVAGTTKAEAEA Db 426 LLFLNSQMPMYIVSITVACAIAFALTYYFGYADKEBDVSAKKPEAPAAAVAGTET QY 300 PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF	ON 360 PSGRAFANETGAEDGSNVDILMHIGEDTVALNGTHFNPLKKGGDEVKAGELLCEFDIDAI 419 Db 536 FGRAFANETGAEDGSNVDILMHIGEDTVALNGTHFNPLKKGGDEVKAGELLCEFDIDAI 419 1	GGSFIFATASMANIAQGAACIAVFELAK GGTALWPMIALSNIAQGSAVFAYSFKHR RWPFFIGIGTAAIGGALIALFNIKAVAL IYPFVAGMTGSALACMLSVTFNVTAASI IYPFVAGMTGSALACMLSVTFNVTAASI IAFCAAIAYGYVKRNGSIDPDATAAF I IAFCAAIAYGYVKRNGSIDPDATAAF I IAFCAAIAYGYVKRNGSIDPDATAAF I IAFCAAIAYGYVKRNGSIDPDATAAF I

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A)Residues: 1-479 <HEI>
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RESULT 12
F95200
PTS system IIABC components [imported] - Streptococcus pneumoniae (strain TIGR4)
PTS system IIABC components [imported] - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95200
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Accession: P95200
A;Accession: P95200
A;Accession: P95200
A;Accession: P95200
A;Accession: Pyer: DNA
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A;Gene: SP1722
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE005672; PIDN:AAK75799.1; PID:g14973217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.1%; Score 664; DB 2; Length 62
larity 34.3%; Pred. No. 9.8e-38;
Conservative 92; Mismatches 187; Indels
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A, Experimental source: strain TIGR4
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Matches 159; Conserv
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A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: B38067
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1.627 < KMR>
A; Residues: 1.627 < KMR>
A; Residues: Sorian Sorian Streptococcus Streptococcus Sorian Streptococcus Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian So
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C.Species: Vibrio cholerae
C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C.Accession: R82432
R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Reterence number: A82035
A;Status: preliminary
A;Molecule type: DNA
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A;Experimental source: serogroup 01; strain N16961; biotype El Tor
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A,Gene: VCA0653
A,Map position: 2
C,Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 AFPAALSAFLGITEPAIFGVNLRFRKPFFLSLIAGAIGGGLASILGLAGTGNGITIIPGT
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Length 479;

DB 2;

Score 659;

27.9%;

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A, Status: preliminary
A, Modecule type: DNA
A, Residues: 1-480 < KIR>
A, Cross-references: UNIPROT: Q99RQ0, GB: BA000018; PID: 913702328; PIDN: BAB43469.1; GSPDB: GA. Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTS system, sucrose-specific IIBC component [imported] - Staphylococcus aureus (strain
                               1;
                                                                                                                                                    61 KRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
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                                                        1 MAMVFPSLVNGYDVAATWAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D90038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMVFPSLVNGYDVAATMAAGE-MPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                               4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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27.9%; Score 659; DB 2; Length 480
Best Local Similarity 48.6%; Pred. No. 1.6e-37;
Matches 139; Conservative 53; Mismatches 82; Indels
                         87; Indels
Best Local Similarity 49.3%; Pred. No. 1.6e-37;
Matches 133; Conservative 46; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                           237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 266
                                                                                                                                                                                                                                                                                                                                                                                  434 PGIISINPQQIGYYIMGMAISFVAAFALTV 463
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Search completed: October 29, 2004, 23:15:05 Job time : 42 secs

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October 29, 2004, 23:14:30 ; Search time 130 Seconds (without alignments) 1167.177 Million cell updates/sec
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1 MAWUFPSLVNGYDVAATWAA.....IEAGANLLNVAKKEAVPATP 468
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Copyright (c) 1993 - 2004
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Maximum Match 100%
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Semience 10. April	Secuence 6404. An	Semience 60875 A	Semence 375. Ann	Semence 13467. A	Semience 367 ann	Semience 73843 A	Semience 253 ann	Semience 74439	Segretary A	Semience (0203), A	Section 26 April	Sequence 43922, A	
SUMMARIES		di :	US-10-450-055-10	US-09-738-626-6404	US-10-282-122A-60875	US-10-474-776-375	US-09-815-242-13467	US-10-474-776-367	US-10-282-122A-73843	US-10-474-776-253	US-10-282-122A-74439	US-10-282-122A-70209	US-09-738-626-6961	US-10-450-055-26	US-10-282-122A-43922	
		DB	15	9	15	16	9	16	15	16	15	15	່ດ	15	15	
	Query	Length	468	199	617	655	627	381	612	612	620	379	683	683	681	
o\r	Query	Match	100.0	100.0	29.4	28.5	27.9	24.8	24.5	24.1	23.9	20.8	19.8	19.8	14.7	
		Score	2363	2363	695	673	099	585	578.5	570.5	564.5	492	468.5	468.5	348.5	
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5658	Sequence 12270, A	10809	Sequence	a)	Sequence 55853, A			12272. A	e 44138.	75030,	equence 75796.		75740,	e 59437.	72912.	53222,	70806,	71894.	13794. 7	e 45789,	5822,	12942	e 71596	525	280	330,	_	e 427	57	45636,
09-815-242-	US-US-815-242-12270 5 US-10-282-122A-51493	US-09-815-242-10809	D	US-10-282-122A-7	-282-1	US-10-282-122A-5	US-10-282-122A-5	315-242-12272	US-10-282-12	US-10-282-1	5 US-10-282-122A-75796	US-10-282-122A-7	US-10-282-122A-7	US-10-282-1	US-10-282-122A-7	10-282-122A-5	US-10-282-1	5 US-10-282-122A-71894		32-12	-24	US-09-815-242-1294	US-10-282	US-10-282-122A-525	US-1	9-741-6	US-09-815-242-10089	5 US-10-282-122A-42726	US-10-282-122A-572	US-10-282-122A-4563
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345.5	345	38.	38.	36.	31.					32	21.	319.5	31	8	16.	315.5	08.	90	305.5	304.5	300	30	299.2	σ.	29	98.		98.	O.	293.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                  APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: No. US20040043953Alel genes of Corynebacterium
FILE REPERBING: 936 2000
CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Vers. 2.0
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Best Local Similarity 100.0%; Pred. No. 1e-195; Length 468; Matches 468; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-450-055-10
              Sequence 10, Application US/10450055
Publication No. US20040043953A1
GENERAL INFORMATION:
US-10-450-055-10
                                                                                                                                                                                                       SEQ ID NO 10
LENGTH: 468
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                                                                                                                                                                                                           2 AMVEPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                 421 AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPATP 468
                                                                                                                                                                                                                                                                                            Length 617;
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34.8%; Pred. No. 3.2e-51;
tive 82; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION TOWNER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-36
PRIOR FILING DATE: 2001-02-36
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60875, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Tyawick, John
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 60875
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Forsyth, R.
Xu, H.
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Best Local Similarity 34.89
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr, Grant
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                                                                                                         241 SIDAPDWVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP 300
                                                                                                                                                                                        301 AEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP 360
                                                                                                                                                                                                                                                                                            SCHAFAVRIKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420
                                                                                                                                                          301 AEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP 360
                                                                                                                                                                                                                                                       SCHAPAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420
                 181 GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV 240
                                                               SIDAPDMYMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAAAP 300
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100.0%; Pred. No. 1.7e-195;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6404, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
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Best Local Similarity
Matches 468; Conserv
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US-09-738-626-6404
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APPLICANT:
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		APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REPERBNCE: ELITRA, 0.11A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2000-03-21 FRICH APPLICATION NUMBER: 60/191,078 PRICH APPLICATION NUMBER: 60/191,078 PRICH APPLICATION NUMBER: 60/207,727 PRICH APPLICATION NUMBER: 60/207,727 PRICH FILING DATE: 2000-05-26 PRICH APPLICATION NUMBER: 60/245,578 PRICH APPLICATION NUMBER: 60/245,578 PRICH APPLICATION NUMBER: 60/253,625 PRICH APPLICATION NUMBER: 60/253,625 PRICH PLING DATE: 2000-10-23 PRICH PLING DATE: 2000-11-27 PRICH PLING DATE: 2000-11-27 PRICH PLING DATE: 2000-11-27 PRICH PLING DATE: 2000-11-27 PRICH PLING DATE: 2000-11-27 PRICH PLICATION NUMBER: 60/253,625	FALOR FILING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 14110 SEQ ID NO 11467 LENGTH: 627 TYPE: PRT TYPE: PRT COGANISM: Streptococcus pneumoniae US-09-815-242-13467	Query Match
QY 62 RLKGTADFLITPVLTLLLTGPLTFIAIGPAMRWVGDVIAHGLQGLYDFGGPVGGLLFGLV 121 :	Qy 293 TKABARAPAEFSNDSTIIQAPLITGBAIALSSVSDAMFASGKIGSGVAIVPTKGQIVSPVS 352 Db 458 TKBAKETGVEAEVIVSPIRGNIVPLNBVKDBAFSAGLIGKGVAIVPQEGKLISPVN 513 Qy 353 GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDBVKAGELLC 412 Db 514 GTIETAFPTGHAIGIRSDKGVEILLHVGFDTVQINGKYFKLLVAQGDRVLVGQALL 569 Qy 413 EFDIDAIKAAGYEVTTPIVVSN 434 Db 570 EFDLEAIKADGYDITTPIVVTN 591	RESULT 4 US-10-474-776-375 Sequence 375, Application US/10474776 Publication No. US20040110181A1 GENUEAL INFORMATION: APPLICANT: Wyeth TITLE OF INVENTION: TITLE O	Query Match 28.5%; Score 673; DB 16; Length 655; Best Local Similarity 35.3%; Pred. No. 2.8e-49; Added to the conservative of the conser	Qy 59 LHKRLKGTADFLITPVITLLIGFITFIAIGPAMRWVGDVLAHGLQGLYDFG-GPVG-114 255 WHKHIPBVISMIEVPFLSLIPALILAHTVLGPIGWTIGQGLSSVVLAGLTGFVKM1 310 Qy 115 -GILFGLVVSPIVITGLHQSFPPIELELF-NQGGSFIFATASWANIAQGAACLAVFFLAK 172

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246 -DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFS 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 SFIFATASMA------NIAQGAACLAVFFLAKSEKLKGLAGASGVSAVL-GIT 192
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PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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PRIOR PILING DATE: 2001-02-06
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRICA APPLICATION NUMBER: 60/191,078
PRICA APPLICATION NUMBER: 60/191,078
PRICA PAPLICATION NUMBER: 60/296,848
PRICA FILING DATE: 2000-03-21
PRICA FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%; Score 578.5; DB 15; Length 33.3%; Pred. No. 3.8e-41; tive 83; Mismatches 143; Indels
                                Sequence 73843, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Streptococcus pneumoniae US-10-282-122A-73843
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                                                                                                                                                                                                                                                                           Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Jud
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                    JS-10-282-122A-73843
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SEQ ID NO 73843
LENGTH: 612
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Best Local
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TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REPERBNCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 LHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 VMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE-APAEFSND 306
                                                                                                                          18 HIYVGNGQLPQYLLMVAVSFALGFALTYMFGY------BDBVDATAAAKQABVAEEKEE 470
                                                                                                                                                                                      299 - APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVV 357
                                                                                                                                                                                                                    471 VAPAALQNETLV--TPIVGDVVALADVNDPVFSSGAMGQGIAVKPSQGVVYALADAEVSI 528
                                                                                                                                                                                                                                                                                     358 AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
                                                                                                                                                                                                                                                                                                                 1 MVTPFVTLLVMSILGLFVIGPVFHVVENYILIATKAILSMPFGLGGFLIGGVHQLIVVSG 60
                                | : :|| |||||||||||||| |||| : : | |||| | :: : | AFPAALSAFLGITEPAIFGVNLRFRKPFFLSLIAGAIGGGLASILGLAGTGNGITIIPGT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 LGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG-VVSIDAPDM
                                                                                               239 VVSIDAPDMVMFLVCAVVTFFIAFGAALAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE
AGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                       24.8%; Score 585; DB 16; Length 3 34.4%; Pred. No. 5.4e-42; rive 82; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                    418 AIKAAGYEVTTPIVVSN----YKKTGPVNTYGLGEIEAGANLLNV 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 367, Application US/10474776; Publication No. US20040110181A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; CRGANISM: Streptococcus pneumoniae US-10-474-776-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.8
Best Local Similarity 34.4
Matches 136; Conservative
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US-10-474-776-367
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### APPLICANITY
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### TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
### FILE REFERENCE: ELITTA.034A

CURRENT APPLICATION NUMBER: U$/10/282,122A

CURRENT FILING DATE: 2000-03-220

### PRIOR PILING DATE: 2000-03-21

### PRIOR PILING DATE: 2000-05-23

### PRIOR FILING DATE: 2000-05-26

### PRIOR FILING DATE: 2000-05-26

### PRIOR FILING DATE: 2000-09-06

### PRIOR APPLICATION NUMBER: 60/230,335

### PRIOR APPLICATION NUMBER: 60/230,335

### PRIOR PILING DATE: 2000-09-06

### PRIOR PILING DATE: 2000-10-23

### PRIOR APPLICATION NUMBER: 60/230,347

### PRIOR PILING DATE: 2000-11-27

### PRIOR PILING DATE: 2000-11-27

### PRIOR PILING DATE: 2000-11-27

### PRIOR PILING DATE: 2000-11-27

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### PRIOR PILING DATE: 2000-10-29

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### PRIOR PILING DATE: 2001-02-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 SPIVITGLHQSFPPIELELFNQGGSFIFATASNA-NIAQGAACLAVFFLAKSEKLKGLAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 PLVVMTGNHWAFAPIFLAASVATPDVLILPAMLASNLAQGAASLAVAFKTKQKQTRQVAL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SIDAP----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 ASGVSAVL-GITEPAIFGVNLRLRMPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 MVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 74439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.9%; Score 564.5; DB 1
30.8%; Pred. No. 6.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74439
                                              Mang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 135; Conservative
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Best Local Similarity
                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 253, Application US/10474776

GENERAL INFORMATION:
APPLICANT: Myeth
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
FILE REFERENCE: AMTIGENS AND USES THEREOF
FILE REFERENCE: AMTOG49-PCT
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SSOFTWARER: Patentin version 3.1
LENGTH: 612
                                                                                                                      424
            NDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DWWMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFS 304
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                                         462 NKKMIF-SPISGEIIPLSDVQDKTFSDKLIGDGVAIIPSEGKVYAPFDGKITNIFPTKHA
                                                                                                         365 FAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGY
                                                                                                                                        27 SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLTGFLTFI
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US-10-282-122A-74439
; Sequence 74439, Application US/10282122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Streptococcus pneumoniae
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Matches 143; Conservative
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ETVTPVIVTN 586
                                                                                                                                                                                                        EVTTPIVVSN 434
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ETVTPVIVTN 586
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US-10-474-776-253
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31; Gaps

Length 620; Indels

DB 15;

297 AEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV 356

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289 PAGTIKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLV 348
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                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFI
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121 VYSPIVITGLHQSFPPIELELFNQ--GGSFIFATASMANIAQGAACLAVFFLAKSEKL--
                                                                                     177 -KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 249-125
CURRENT APPLICATION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6961
                                                                                                                                                                                                                     330 VGGVPAFISIQKEFWPVYLIATAIALAV 357
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US-09-738-626-6961
                                                                                                                                                                                                                                                                                                                               Sequence 6961, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HARASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.8%
Matches 141; Conservative
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IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                               US-09-738-626-6961
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
             SQVKSGLSTKQT-LYAPMTGEMLFLSEVPDETFSSKLLGEGFAILPSEGEVYAPFDGEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 16; Gaps
                                                                                   - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
20.8%; Score 492; DB 15; Length 379;
Best Local Similarity 37.3%; Pred. No. 5.9e-34;
Matches 100; Conservative 63; Mismatches 89; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                               ; Sequence 70209, Application US/10282122A ; Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; CRGANISM: Staphylococcus aureus; US-10-282-122A-70209
                                                                                                                                                  DAIKAAGYEVTTPIVVSN 434
                                                                                                                                                                        577 DFITSKGYSLISPVVVTN 594
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-70209
                      462
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APPLICANT:
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US-10-282-122A-43922
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APPLICANT:
APPLICANT:
APPLICANT:
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SPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAG 408
                 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 LLGPFGIGVGNGISNLLEAINNFSPFILSIVIPLIYPFIVPLGLHWPLNAIMIQNINTLG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGAS--GVSAVL--GITEPAIFGVNL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 YDFIQGPMGAWNFACFGLVTGVFLLSIKERNKAMRQVSLGGMLAGLLGGISEPSLYGVLL 397
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                                                               461
                                                                            BLLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK 461
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Publication No. US20040043953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: No. US20040043953A1e1 genes of Corynebacterium
FILE REFERENCE: 936 2000
CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT PILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Vers. 2.0
LENGTH: 683
                                                       409 ELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
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                                                                                                                                                                                                                                                                                                                                                                                                         19.8%; Score 468.5; DB 1
llarity 29.8%; Pred. No. 1.5e-31,
Conservative 79; Mismatches 206
                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-450-055-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 FGAAIAYGLYLVRRNGSID-----
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                  RESULT 12
US-10-450-055-26
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349
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Best Local S
Matches 141
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Sequence 43922, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos APPLICANT: Malone, Cheryl

US-10-282-122A-43922

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 DKQSQAVTASATELPYAVLEAMGGKANIKHLDACITALRVEVNDKSKVDVPGLKDLGASG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 VLEVGNNMQAIFGPKSDQIKHEMQQIMNGQVVENPTTWEDDKDETVVVAEDKSATSELSH 533
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFL----ITPVLTLLLTGF
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Best Local Similarity 24.4%; Pred. No. 3.5e-21;
Matches 133; Conservative 67; Mismatches 192; Indels 153; Gaps

    See File Wrapper or PALM.

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PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-12-22

PRIOR PILING DATE: 2001-02-09

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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                             Carr, Grant
Yamamoto, Robert
Forsyth, R.
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83 LTFIAIGPAMRWVGDVIAHGLQGLYDFGGPVGGILFGLVYSPIVITGLHQSF 134 : :			172 KSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 227	297 KPENKKVVAGIMGSAALISFLIGITEFLEFSFLFVAPLLFFIHAVLDGLSFLTLYLL 353	228 AVALGAAGFLGVVSIDA-PDMVMFLVCAVVTFFI 260	354 DVHLGYTFSGGFIDYVLLGVLPNKTQWMLVIPVGLVYAVIYYFVFRFLIVKLKXKTPGRE 413	261AFGAAIAYGLYLVR274	414 DKOSQAVTASATELPYAVLEAMGGKANIKHLDACITRLRVEVNDKSKVDVPGLKDLGASG 473	275RNGSIDPDATAAPVPAGTIKAEABAPAEFSNDST 308	474 VLEVGNNNQAIFGPKSDQIKHEMQQIMNGQVVENPTIMEDDKDETVVVAEDKSATSELSH 533	SGKLGSGVAIVE	534 IVHAPLTGEVTPLSEVPDQVFSEKNMGDGIAIKPSQGEVRAPFNGKVQMIFFPKHAIGL- 592	369 TKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTT 428	593VSDSGLELLIHIGLDTVKLNGEGFTLHVERGQEVKQGDLINFDLDYIRNHAKSDIT 649	429 PIVVS 433	650 PIIVT 654
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Run on:

October 29, 2004, 23:06:04; Search time 39 Seconds (without alignments) 795.816 Million cell updates/sec

Perfect score:

US-09-604-231-2 2363 1 MAWVFPSLVNGYDVAATMAA.....IEAGANLINVAKKEAVPATP Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

478139 segs, 66318000 residues Searched:

Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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	Length		496	627	628	655	656	670	583	612	634	631	316	243	427	526	483	590	481	475	478	969	726	635	929	688	482	585	482
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	Score	i	•	w	w	9	•	$^{\circ}$	583.5	72.	26	•	23		01.	97.	∞	4.1	63.	357.5	36.	02	20	•	ത	σ	œ	ထ	<u> </u>
	sult No.		⊣ .	2	m	4	ហ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	T 6	20	21	22	23	24	25	26	27

Sequence 5773, Ap		Sequence 368, App		9162, #	18115,	10571,		Sequence 5592, Ap	Sequence 4040, Ap	Sequence 352, App	3693,				
US-09-543-681A-5773 US-09-134-001C-3134	US-09-107-532A-5798	US-09-543-681A-7659	US-09-134-000C-3657	US-09-489-039A-9162	US-U9-252-991A-18115	US-U9-489-039A-10571	US-09-107-532A-4365	US-09-107-532A-5592	US-09-583-110-4040	US-09-492-709A-352	US-09-134-000C-3693	US-09-583-110-5074	US-09-107-532A-5352	US-09-252-991A-19278	US-09-134-001C-4303
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269.5	266.5	256	248	44.0	200	101	101.0	T 1	157	151.5	144	141.5	139.5	137	136.5
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ALIGNMENTS

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Sequence 5822, Application US/09134000C

Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: BYTENCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BYTENCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNGE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 5322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecalis
US-09-134-000C-5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: EDCE:
US-09-134-000C-5822
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Query Match
Best Local Similarity 39.3%; Pred. No. 2.4e-75;
Matches 184; Conservative 84; Mismatches 171; Indels 29

7;

29; Gaps

174 61 KRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFGL 120 234 09 95 1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 121 VYSPIVITGLHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE KLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 175 156 47 216 gg δ 원 g δ ð g

GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK 294 295 AEAEAPAEFSNDSTI--IQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS 352 334 INTNQIANADEPTTVETIVSPLAGEITTLGSVNDPVFSSESIGKGIAIKPNGNTIYSPVD 393 235 q à ₹ g

353 GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG--DEVKAGEL 410

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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE:
FOR INVENTION NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
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PRIOR APPLICATION NUMBER: US 60/081,553
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PRIOR PRIOR APPLICATION NUMBER: US 60/051,553
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 394 GIVQVVFETGHAYDLKS----NTGAEILLHVGIDTVSLNGKGFT--KKVGAKQKVKKGEV 447
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                                                      411 LCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNV 458
                                                                          448 LGTFDSTVITNSGLDDTTMVIVTNSKDYSBVIPITKNIVTBGAALLTI 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.3%; Score 669; DB 4; 34.5%; Pred. No. 1.2e-58;
                                                                                                                                                                              Sequence 3124, Application US/09583110 Patent No. 6699703
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                                                                                                                                                                   US-09-583-110-3124
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US-09-583-110-3124
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LENGTH: 627
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Matches
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RESULT 3 US-09-107-532A-5288 'S-Squence 5288, Application US/09107532A ', Patent No. 6583275

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 VSLLTIPTFINTVDGVESNVTVAVIATGIAFVLAFVGTLILGFDEQTQDNQLE----- 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 TKLRALGISSTVTSLFGITEPTVYGVTLPLKKPFIAACISGGIGGAIIGFSGVKAFSSSL 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 EKLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA--- 230
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                                                                             NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...628
; SEQUENCE DESCRIPTION: SEQ ID NO: 5288:
US-09-107-532A-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                              STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 628 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (781)893-8277
                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                        CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Sequence 8112, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/95/134,000C
CURRENT FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4606
LENGTH: 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 WOVCVIFGLHWGLVPLMINNMTVLGHDSMLPIILPAVIAOVGAVLGIFLATRDARORVLA 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 GFLGVVSIDAP-----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 -----GAVIVAPAS-AND---ILAPMSGSVIALEQVPDSTFASGLLGKGVAIIPAVGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 VSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 QMIPPGGIDASVWGGLIGTGVAFVLACVLTFFA-----GL-----PRGSAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 GELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.5%; Score 626.5; DB 4; Length Best Local Similarity 33.5%; Pred. No. 2.6e-54; Matches 158; Conservative 82; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4606, Application US/09134000C
Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
         JS-09-489-039A-8212
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-8212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-134-000C-4606
                                                                                                                                                                                                                                                                                                                  SEQ ID NO 8212
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Patent No. 6699703

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Prenumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Prenumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: PATHOLO-07A

CURRENT PELING DATE: 2000-05-26

PRIOR PILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

PRIOR FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 2958

LENGTH: 655
                                         348 VSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKOGDEVKA 407
                                                                      -----NKHANAGEPITSARHTLKSPLTGKVLPLSEVPDQVFSSGVMGKGIAIDPEVGEL 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LHKRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFG--GPVG-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 WRKGIPEVISMIFVPFLSLIPALILAHTVLGP----IGWTIGQGLSSVVLAGLIGPVKWL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 SEKLKG-LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGFLGVVSIDAPDMVMF----LVCAVVTFFIAFGAAIAYGLYLVRRNG---SIDPDAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIGGLPGILSİQPQYMLPPAGTMLVAIVVPMLLTP------FPRKAĞLFTKİEGDTN 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     885 AAPVPAGTTKAE--AEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOABFVAQEEABFVSHEPVELT--SVEIISPLTGQVKELSQATDPVFASGVMGQGLVIEP 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQGELTSPVNGTVTVLPPTKHAIGI--VSDEG--VELLIHIGMDTVGLDGKGFESLVVQG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKK----TGPVNTYGLGEIEAGANLL 456
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                                                                                                                                                                       1 MAMVFPSLVNGYDVAATMAAGEMP--MWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.7%; Score 655; DB 4; Length 655;
Larity 34.4%; Pred. No. 3.4e-57;
Conservative 91; Mismatches 177; Indels
                                                                                                                                                                576 GDLLIRFDIEAIRAAGYSVITPVVITN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 165; Conserv
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  466
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Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
Pneumoniae for Diagnostics and Therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIKGLAGASGVSAVLGITEPAIFGVNURLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNG---SIDP--DATAAPVP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LSSVSDAMFASGKL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 LQTANGATATPQSFEPVSA-----TGTAVATKETLFAVAAGTIKBITEVNDPVFSQRMM 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTH 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 GDGYAVEPSNGKVYAPVNGKVTSVFETKHAIGILS----NBGLEVLVHMGLDTVELKGVP 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KRIKGTADFLITPVLTLLITGFLTFIAIGP----AMRWVGDVLAHGLQGLYDFGGPVGGL
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.1%; Pred. No. 4.8e-50;
Matches 139; Conservative 100; Mismatches 194; Indels 45
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CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US/09/107,433
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-05-12
PRIOR PELICATION NUMBER: US 60/085,131
PRIOR PELICATION NUMBER: US 60/085,131
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1997-07-02
                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
;
; LOCATION: (B) LOCATION 1...583
; SEQUENCE DESCRIPTION: SEQ ID NO: 681
US-09-107-532A-6811
                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2911, Application US/09583110 Patent No. 6699703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al. TITLE OF INVENTION: Nucleic Acid and TITLE OF INVENTION: Preumoniae for Di
                       TELECOMMUNICATION: INFORMATION:
TELEPHONE: (781)893-5007
REFERENCE/DOCKET NUMBER:
                                                                                INFORMATION FOR SEQ ID NO: 6311:
SEQUENCE CHARACTERRISTICS:
LENGTH: 583 amino acida
TYPE: amino acid
                                                          TELEFAX: (781)893-8277
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-583-110-2911
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                        FLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                398 FKLKDKKLKALCPPAIISGIFGVTEPAIYGITLPKKWPFIYSMIGGAVGGLYLMINNVTA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 VALGAAGFLGVVSI----DAPDMVMFLVCAVVTFFIAFGAAIAYGL-YLVRRNGSIDPDA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557
                                                                                                                                                                                                 WILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDF 109
                                                                                                                                                                                                                                                                                        278 AFAÀQVQKVFKRIIPEVVQTFLVPFFVLLIALPIGFLVIGPIVSMLTDLLSAGFTALMSF 337
                                                                                                                                                                                                                                                                                                                                            GGPVGGLLFGLVYSPIVITGLHOSFPPIELFNQGGSFIFATASM-ANIAQGAACLAVF 168
                                                                                                                                                                                                                                                                                                                                                                                 SPALYGLILGFFWQVLVIFGLHWSVVPLAIMQVTQEGSSQVLFGSFAASFAQTAVVLAMF 397
                                                                                                                                                                       ---AQAGYQGTVLPVLVVS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 TAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNFLKKQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 EVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                         Length 670;
                                                                                                                                85; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: GENOME THERAPBUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                       2 AMVFPSLVNGYDVAA---TMAAGEMPMWSLFGLDV---
                                                                                         25.8%; Score 609; DB 4; 30.9%; Pred. No. 1.6e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: CD/ROM 1SO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6811, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
STATE: Massachusetts
                                Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                Best_Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-107-532A-6811
                                                      US-09-134-000C-4606
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                                                                                               Query Match
                                    ORGANISM:
               TYPE: PRT
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Sequence 3902, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF ENTEROCOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
           238 RIVPEMVKVEMVPLLVILVSTPIALIAVGPVTSWFAQLIADGVILIQEHTGFIAIPLLVA 297
                                                                                                                                                              234 AGELGV---VSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAFV-- 288
                                                                                                                                                                                                                                                                                                                                                                 VAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKABDGSNVDILMHIGFDTVNLNGTHFNP 397
                                                                                                                                                                                                                                                                                                                                                                                      VYSPIVITGLHQSFPPIELELFNQGG--SFIFATASMANIAQGAACLAVFFLAKSEKLKG
                                                                                        464 EEENNKQAASTNKKPQIANSKLPVG-----LISPLQGKTVALSEVNDETFASGIMGPG
                                                                                                                                             LAGASGVSAVL-GITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALF----NIKAVALGA
                                                                                                                                                                                                                                                       414 PGLLSLPMWIS-DTDNQV---VNAIITLLIASVATFIATLII----GFDDP--TDDPIRD
                                                                                                                                                                                                                                                                                          -----PAGTTK----AEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSG
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CORRESPONDENCE GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVVKGQKVTKGDTLIBFDLDAIIAAGYDFTTMIIITN 609
                                                                                                                                                                                                                                                                                                                                                                                                                                           398 LKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 434
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 631 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3902:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Patent No. 6605709
Batent No. 6605709
Batent No. 6605709
BAPILICANT: GRAY BRETON
TITLE OF INVENTION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
                                                                                                                                                                           12;
                                                                                                                                                                                                                            87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 SFIFATASMA------NIAQGAACLAVFFLAKSEKLKGLAGASGVSAVL-GIT 192
                                                                                                                                                                                                                                                                                                                                                                                      --IFLAASIATPDVLILPAMLGSNLAQGAASMAVALKSKNNNTKQIAFAAGFSALLAGIT 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 -DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPARFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHA
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                                                                                                                                                                                                                                                                                                       256 VVGPIGVIVGEGLSNLVGQMYGVAGWLTLAILGAIMPFIVMTGMHWAFAP----
                                                                                                                                     Length 612;
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                                                                                                                                                                          Indels
                                                                                                                                     DB 4;
                                                                                                                             24.2%; Score 572.5; DB 4
33.3%; Pred. No. 6.7e-49;
tive 81; Mismatches 145
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                                                                     ORGANISM: Streptococcus pneumoniae
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     5322
                                                                                                                             Query Match
Best Local Similarity 33.3
Matches 143; Conservative
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Best Local Similarity 32.8
Matches 150; Conservative
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   SEQ ID NOS:
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                                                                                          US-09-583-110-2911
NUMBER OF SEQ
SEQ ID NO 2911
LENGTH: 612
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Sequence 5530, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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US-09-134-001C-4114
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| Patent No. 6617156
| GENERAL INFORMATION:
| PAPPLICANTY: Lynn Doucette-Stamm et al
| TITLE OF INVENTION:
| TITLE OF INVENTION:
| RICHERFERENCE: 032796-032
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT APPLICATION NUMBER: US/09/134,000C
| PRIOR APPLICATION NUMBER: US 60/055,778
| PRIOR APPLICATION NUMBER: US 60/055,778
| PRIOR FILING DATE: 1997-08-15
| NUMBER OF SEQ ID NOS: 6612
| SEQ ID NO 5482
| LENGTH: 316
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                                                                                                                                                                                  7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 412
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                                                                                                                                                                                                                                                                 ALVYPTIVSAYSDSITL-----RFLGMPVILARYTSTVIPALLAVWLSYIBPKIKK 260
                                                                                                                                                                                                                                                                                                                                                RLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFGLV 121
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                                                                                                                                                                                                                                          2 AMVEPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK
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                                                                                                                                  DB 4; Length 631;
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                                                                                                                                                                                    84; Mismatches 169;
                                                                                                                                  Score 562.5; DB 4
Pred. No. 7.2e-48;
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...631
SEQUENCE DESCRIPTION: SEQ ID NO: 3902:
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                                                                                                                                  23.8%;
ilarity 30.3%;
Conservative 8
                                                                                                                                       Query Match
Best Local Similarity
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US-09-134-000C-5482
                                                                                    US-09-107-532A-3902
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APPLICANT: LINCONCATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BLIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PLILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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                                                                                                                                                                                                FFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKABAB---APAEFS-NDSTIIQAP 313
                                                                                                                                                                                                                                                                                                                     FIJAFVLT-----FVLRFEDQPNPE-----TATEKTETDKMVAPVKTNQEDKIILASP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGBAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRIKAED 373
66 KKPFIAACIGGGIGGAFVANNHVKNPTFGLVSMLSLPGFIPAETKDTAPMITGAIGAGIA 125
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48.2%; Pred. No. 2.9e-44;
iive 42; Mismatches 57
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Sequence 4715, Application US/09134000C

Patent No. 667156
GENERAL INFORMATION:
APPLICANT: Lynn boucette-Stamm et al
TITLE OF INVENTION: BNTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BNTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: 1999-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SCPTWARE PATENTIN Version 3.1
SEQ ID NO 4715
                                                                                                                                                                                                                                                                                                                                                                                                        21.1%; Score 497.5; DB 4; 29.4%; Pred. No. 2e-41; tive 87; Mismatches 183;
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US-09-489-039A-13018
                                            US-09-134-000C-4715
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                     MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...427

SEQUENCE DESCRIPTION: SEQ ID NO: 5530:
US-09-107-532A-5530
                                                                                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5530:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
                                   CITY: Waltham
STATE: Massachusetts
                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Matches 124; Conservative
                                                                       COUNTRY: USA
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Sequence 13018, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                          114 GGLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAK 172
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                                                                                                                                  54 TIBKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLOGLYDFGGPV
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                                                                                              1 MAMVFPSLVNGYDVA-----ATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILA
                                                   Gaps
                                                49;
Length 526;
                                                   Indels
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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120 LVYSPIVITGLHQSFPPPIELELFNQ---GGSFIFATASWANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                                              213 LTHPALTNAWGVAAGFHTM------NFFGIEVAMIGYQGTVFPVLLAVWFMSNVEKRL 264
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                                                                                                                                          3 MVFPSLVNGYDVAA---TMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                                  Query Match

20.7%; Score 489; DB 4; Length 483;
Best Local Similarity 38.5%; Pred. No. 1.3e-40;
Matches 104; Conservative 51; Mismatches 101; Indels 14; Gaps
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13018
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Search completed: October 29, 2004, 23:15:53 Job time: 41 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
              Copyright
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OM protein - protein search, using sw model

Run on:

October 29, 2004, 22:57:48; Search time 156 Seconds (without alignments) 1076.188 Million cell updates/sec

US-09-604-231-2

Title: Perfect score:

2363 1 MAWYFPSLVNGYDVAATWAA.....IEAGANLINVAKKEAVPATP 468 Sequence:

Scoring table:

2002273 segs, 358729299 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Genesed Database

geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* 23Sep04:* geneseqp2004s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aab66707 C.clutami		; ;									Abb49833 Listeria			; t						ייי					
CHINATIO	ID	AAB66707	ABG80325	AAG92650	AAB69080	AAB66708	ADH87937	ABB47495	ABU32951	ABU02378	ABP81458	ADK46609	ABB49833	ABP25654	ADC95661	AAU37874	ABM72990	ADK46443	ABP25655	ABP27216	ABB49923	ABO61695	ADH86721	ABP27215	ABB54803	ABP81450	
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ALIGNMENTS

AAB66707 standard; protein; 468 AA. RESULT 1 AAB66707

AAB66707;

(first entry) 09-APR-2001

#1. C.glutamicum phosphoenolpyruvate protein Phosphoenolpyruvate; sugar phosphotransferase system; PTS.

Corynebacterium glutamicum

WO200102583-A2.

11-JAN-2001

27-JUN-2000; 2000WO-IB000973

99US-0142691P. 99US-0150310P. 99DE-01042095. 99DE-01042097. 01-JUL-1999;

23-AUG-1999; 03-SEP-1999; 03-SEP-1999;

(BADI) BASF AG.

Zelder O, Haberhauer G; Schroeder H, Pompejus M, Kroeger B,

WPI; 2001-080989/09.

Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.

Claim 4; Page 101-102; 144pp; English.

The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation

Sequence 468 AA;

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Pred. No. 1.2e-226;
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             Local Similarity
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New metabolic pathway genes of Corynebacterium glutamicum for producing

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fine chemicals, e.g. lipids, (un)saturated fatty acids, vitamins, cofactors or enzymes used in food, feed, cosmetics or pharmaceutical
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                                                                  Claim 18; Page 111-113; 176pp; English.
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                     mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO 6404; 246pp + Sequence Listing; English.
                                                                                                                              16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
                                                                                            18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                          KYOW ) KYOWA HAKKO KOGYO KK
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Senoh A, I
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                  EP1108790-A2
                                                                                                                                                                                                                                                 Nakagawa S,
Tateishi N,
                                                        20-JUN-2001
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Sequence 661 AA;

0; Gaps Query Match 100.0%; Score 2363; DB 4; Length 661; Best Local Similarity 100.0%; Pred. No. 2.1e-226; Matches 468; Conservative 0; Mismatches 0; Indels 0;

120 253 9 1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 61 g ò 엄

> ð 셤 ğ 임 δ g õ

SGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420 SGHAFAVRTKAEDGSNVDILMHIFFFFFFFFFFFKKQGDEVKAGELLCEFDIDAIK 613 AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP 494 361

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à g 421 AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPATP 468

661

AAB69080 standard; protein; 661 RESULT 4

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11-SEP-2003 20-APR-2001

AAB69080;

(revised)
(first entry)

Ë Yokoi

Ochiai K,

H, Ando S, Hayashi M, Ikeda M, Ozaki A;

Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system. Brevibacterium lactofermentum sucrose PTS enzyme II protein SBQ ID

Corynebacterium glutamicum

WO200102584-A1

30-JUN-2000; 2000WO-JP004348.

99JP-00189512 02-JUL-1999;

(AJIN) AJINOMOTO CO

Kurahashi O; Nakamatsu T, Sugimoto M, Izui M,

WPI; 2001-138150/14. N-PSDB; AAF32543

Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding

Claim 1; Page 29-32; 45pp; Japanese.

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The present sequence represents the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system] enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved aminodistrupted gene, such as one without the sucrose PTS gene and it's to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 661 AA;

253 9 1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 194 MANVFPILVNGYDVAATMTAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 61 KRIKGTADFLITPVLTLLIGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFGL Gaps ; Length 661; Indels Score 2332; DB 4; Pred. No. 2.6e-223; 4; Mismatches 3; 98.7%; Best Local Similarity 98.5 Matches 461; Conservative Query Match 엄 à ð

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120

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à dd

373 VYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180 us-09-604-231-2.rag

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YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIBLELFNQGGSFIFATASMANIAQGAACLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to Corynebacteium glutamicum phosphoconolpyruvate: sugar phosphocransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation
                                            300
                                                                                                            AEFSNDSTIIQAPLIGEALALSSVSDAMFASGKLGSGVALVPIKGQLVSPVSGKIVVAFP 553
                                                                                                                                      SGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420
                                                                                                                                                          SGHAFAVRÍKAEDGSNVDILMHIGFDTVNINGTHFNPLKKQGDEVKAGELLCEFDIDAIK 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
           AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
                                            SIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP
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                                                                                                                                                                                 AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLMVAKKEAVPATP 468
                                                                                                                                                                                                Haberhauer
                                                                                                                                                                                                                                                                                                                                                           Phosphoenolpyruvate; sugar phosphotransferase system; PTS
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                                                                                                                                                                                                                                                                                                                                     C.glutamicum phosphoenolpyruvate protein #2
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                                                                                                                                                                                                                                                                  AAB66708 standard; protein; 362
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99US-0150310P.
99DE-01042095.
99DE-01042097.
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                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum
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03-SEP-1999;
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Gaps

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Indels

77.1%; Score 1821; DB 4; 1 ilarity 100.0%; Pred. No. 1.1e-172; Conservative 0; Mismatches 0;

Best Local Similarity Matches 362; Conserv

Query Match

Length 362;

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The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector
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for diagnosing or
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                                                                                                                                                   PVPAGTTKAEBAEBABFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ
                                                                                                                                                                      VPFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI
                                                                                            KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA
                                                                                                                KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA
VFFLAKSEKLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis infection; transcription regulatory element; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis polypeptide #2417
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N-PSDB; ADH84532.
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Nov

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KRLKGTADFLITPVLTLLIGFLIFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
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comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Entercoccus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
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Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 AEABRABEFSNDSTI--IQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                    35.2%; Score 832.5; DB 7; 39.3%; Pred. No. 9e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Mismatches 171;
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                                                                                                                                                                                                                                                                                        Sequence 496 AA
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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
t are useful for selecting probes and primers for detecting genes in L.

control of the control of the present sequence is a protein
control of the genome sequence of the present invention. Proteins
concoded by the genome sequence are useful for raising specific
antibodies, identification of L. monocytogenes and related organisms, and
for biosynthesis and biodegradation, especially biosynthesis of vitamin

CC antibodies, identification of L. monocytogenes and related organisms, and
EL. The genome sequence and proteins encoded by it are also useful for
call ompounds that regulate gene expression and cell replication
and modulate L. monocytogenes-related diseases. In addition, the genome
cc and modulate L. monocytogenes-related diseases. In addition, the genome
cc sequence and proteins encoded by it are useful in pharmaceutical and
caccines compositions for the treatment or prevention of infections by L.
cmonocytogenes and related organisms. Note: The sequence data for this
controlic format directly from MIPO at
the wine in the Aminished organisms of the wine or the was obtained
the wine in the Aminished organisms.
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                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
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Garrido-Garcia P, Tierrez-Martinez A, Amend A;
on E, Hain T, Berche P, Charbit A, Durant L;
ro F, Garcia Del Portillo F, Gomez-Lopez N;
os B, Wehland J, Kaerst U, Entian K, Hauf J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 IFIGKGFVGFILGIAVAYILSAIGTYFFGYKDEMADGI----
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                                                                                                                                                                                                                                       Claim 6; SEQ ID NO 200; 192pp; French.
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EFDLEAIKADGYDITTPIVVTN
Dominguez-Bernal G, Garri
Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
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Matches 154; Conservative
                                                                                                                    WPI; 2002-010914/01.
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Best Local Similarity
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ω RESULT Length 617;

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the invention tenates to an instract actual computation and pure invention tenates to an instract actual completes of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypoptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense confisced coid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular or proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or the gene product or that has an activity against a biological pathway or proliferation; (7) identifying a compound that influences the activity of identifying a gene required for callular proliferation or the biological pathway or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound; activity; (11) a culture compound that inhibits proliferation of an organism acts; (13) identifying the target of a compound that inhibits the crompound organism; or (13) identifying the target of a compound that inhibits the crompound organism; or (13) identifying the target of a compound that inhibits of compounds or screening for homologous nucleic acids required confident proverse andidate molecules for rational and any acceptance or includes acids are useful for any proverse proverse andidates molecules for a genine and acids are useful for any proverse proverse and acceptance or and acids are useful for any proverse proverse and acceptance or and acids are useful for any proverse proverse and acceptance or and acids are useful for any proverse proverse proverse and acceptance or acids are useful for any proverse proverse prover
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening
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                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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0
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated nucleic acid comprising any
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Forsyth RA,
                                                                                                                                                                                                                                              encoded by Prokaryotic essential gene #18478.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 60875; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                 ABU32951 standard; protein; 617 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-029926
N-PSDB; ACA36821
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25-OCT-2001;
08-FEB-2002;
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                                                                                                            ABU32951;
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                                                                                                                                                                                                                                                                                               457
                                                                                                                                                                                                                                                                                                                         TKABABAPABFSNDSTIIQAPLTGBAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS 352
                                                                                                                                                                                                                                                                                                                                                                           GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 412
                                                                                                                                                                                                                                                                                                                                                                                            ALVYPTMINLFNEGAHITFLQIP------VVLMSYSFSVIPILLAVWFLSILERFLNS 236
                                                                                                                       RIKGTADFLITTPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
                                                                                                                                                                                                                                                                                                                                       122 YSPIVITGIHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
                                                                                                                                                                                                                                                                   ----GVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGT
                                                  2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK
                                                                                                                                                                                                                 181 GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL---
                          Gaps
                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. pneumoniae type 4 strain protein from coding region #1956.
                                                                                                                                                                                                                                                                                     417 IFIGKGFVGFILGIAVAYILSAIGTYFFGYKDEMADGI----
                            82; Mismatches 162;
29.4%; Score 695; DB 6; 34.8%; Pred. No. 6.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; type 4 strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EFDIDAIKAAGYEVTTPIVVSN 434
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EFDLEAIKADGYDITTPIVVTN
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(GENO-) INST GENOMIC RES.
 Query Match
Best Local Similarity 34.88
Matches 154; Conservative
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11-FEB-2003
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Claim 1; SEQ ID NO 3912; 56pp; English.

The invention relates to a protein computers, identified in the identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regalons from the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regalons from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence contained within a Streptococcus nucleic acid sequence. The first primer is substantially complementary to the complement of sequence contained within a Streptococcus nucleic acid sequence to the target sequence, and where the parts of the primers having substantial complementarity define the termin of the target sequence to protein, and determining where the termin of the target sequence to protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes conding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful for identifying encoding the proteins and antibiotics. The methods are useful for identifying tention or more genes or infection. They are also useful in developing vaccines, and antibiotics. The methods are useful for identifying expressed by the identified coding regions from the genomic sequence. Specification, but was obtained in electronic format directly from WIPO at Eth. Publybublished pot sequences. (Updated on 23-OCT-2003 to

Sequence 655 AA;

Length 655; 28.5%; Score 673; DB 6; Length 65 35.3%; Pred. No. 1.1e-57; ive 87; Mismatches 173; Indels al Similarity 35.3 170; Conservative Query Match Best Local 8 Matches

1 MAMVFPSLVNGYDVAATMAAGEMP--MWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKF Gaps 52; à qq

> 8 ρp δ 셤

-GLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAK 172

-SEKLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 173

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GAAGFLGVVSIDAPDWVMF----LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP 288 VPAGTIKAEAE----APAEFSNDSTI-----IQAPLIGEAIALSSVSDAMFASGKLGSG GIGGLPGILSIQPQYMLPFAGTMLVAIVVPMLTF------FFRKAGLFTK----232 431

338 VAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP 397

-TEGDTNLQAEFVAQEEARFVNHEPVELTSVEIISPLTGQVKELSQATDPIFASGVMGQG

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LKKQGDBVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGAN 454 398

New Streptococcus pneumoniae polynucleotides, useful for treating or preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. Streptococcus pneumoniae, infection, otitis media, antibacterial; diagnosis, gene therapy. Russell Streptococcus pneumoniae polypeptide SEQ ID NO 375. Chakravarti DN, Claim 42; Page 617-620; 1091pp; English. AA. Green BA, ABP81458 standard; protein; 655 12-APR-2002; 2002WO-US011524 16-APR-2001; 2001US-0283948P 18-APR-2001; 2001US-0284443P (AMCY) AMERICAN CYANAMID CO (first entry) Streptococcus pneumoniae. Zagursky RJ, Masi AW, WPI; 2003-093010/08. N-PSDB; ABZ42306. 455 LL 456 |: 649 LM 650 WO200283855-A2 04-MAR-2003 24-OCT-2002 Wooters JL; ABP81458: RESULT 10 ABP81458 g à

DP;

a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polymucleotide or a nucleic acid sequence 95% identical to one of the polymucleotides. The S. pneumoniae polymucleotides and encoded polympeptides (ABPR1299-ABPR1674) are useful for treating or preventing S. are induced or exacebateed by S. pneumoniae. These are also useful for pneumoniae in a biological sample or diagnosing S. pneumoniae in a biological sample or diagnosing S. pneumoniae in a subject. The polymucleotides have antibacterial activity and are useful in gene therapy The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of

Sequence 655 AA;

1 MAMVFPSLVNGYDVAATMAAGEMP--MWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKF 52; Gaps Length 655; 28.5%; Score 673; DB 6; Length 65: 35.3%; Pred. No. 1.1e-57; ive 87; Mismatches 173; Indels Query Match
Best Local Similarity 35.3%
Matches 170, Conservative

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114 -GLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAK LHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFG--GPVG--59 115

173 -SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 231 Length 627;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypeptides. The nucleic acids and proteins are useful for diagnoshing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                      LKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGAN 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
              430
                                                                                                                                                     VAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP
                                      GAAGFLGVVSIDAPDMVMF----LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                                      VPAGTIKARAE----APAEFSNDSTI-----IQAPLIGEAIALSSVSDAMFASGKLGSG
                                                             ---FFRKAGLFTK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae protein, Seq ID No 3124
                                                             431 GIGGLPGILSIQPQYMLPFAGTMLVAIVVPMLLTF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
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98US-0085131P.
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segdata.uspto.gov/sequence.html

Sequence 627 AA

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                                                      09
                                                                                                                                                                                                                                                                                                                                                                                                  358 AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID
                                                                                                                                                                                                                                                                                                                                                          KRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                     1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                              182 MMLVSGSLPNAWAVA---QGGEVTAMNFFGF-IPVVGLQGSVLPAFIIGVVGAKFEKAVR
                                                                                                                                                                   VYSPIVITGLHQSFPPIBLELFNQGGSFIF-ATASMANIAQGAACLAVFFLAKSEKLKGL
                                                                                                                                                                                                                          AGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG-
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIKAAGYEVITPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                            92; Mismatches 186;
Score 669; DB 8;
Pred. No. 2.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vitamin B12; bacterial infection; disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes protein #2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB49833 standard; protein; 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2001; 2001WO-FR001118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000FR-00004629
    28.3%;
34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-010914/01
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200177335-A2.
     Query Match
Best Local Simil
Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB49833;
                                                                                                                                                238
                                                                                                                                                                            121
                                                                                                                                                                                                        298
                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                               358
                                                                                                                                                                                                                                                                                                                      418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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The present invention relates to the genome sequence of Listeria

CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.

CC monocytogenes and related organisms, and for studying genets in L.

CC polymorphisms and other genomes. The present sequence is a protein

CC polymorphisms and other genome sequence of the present invention. Proteins

CC polymorphisms and other genome sequence of the present invention. Proteins

CC polymorphisms and biodegradation, especially biosynthesis of vitamin

CC antibodies, identification of L. monocytogenes and related organisms, and

El2. The genome sequence and proteins encoded by it are also useful for

CC selecting compounds that regulate gene expression and cell replication

CC sequence and proteins encoded by it are useful in pharmaceutical and

CC and modulate L. monocytogenes-related diseases. In addition, the genome

CC sequence and proteins encoded by it are useful in pharmaceutical and

CC vaccines compositions for the treatment or prevention of infections by L.

CC monocytogenes and related organisms. Note: The sequence data for this

CC patent did not form that from MIPO at

CC in electronic format directly from MIPO at

CC in electronic format directly from MIPO at

CC in electronic format directly from MIPO at

CC in electronic format directly from MIPO at

CC in electronic format directly from MIPO at
                                  Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                        Claim 6; SEQ ID NO 2538; 192pp; French.
                                      Genomic sequence for Listeria
                                                                                                        polypeptides.
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Sequence 634 AA,

284 TAAPVPAGTIKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPT Gaps 42; Length 634; 172; Indels 28.2%; Score 667; DB 5; 34.6%; Pred. No. 4.3e-57; tive 81; Mismatches 172 578 VIEKGQLLTEFDIEGIKAAGYDVTTPVVVTN 608 EVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 434 Conservative Query Match Best Local Similarity Matches 156; Conserva 56 116 302 362 235 422 344 479 404 d à a g δ 8 g à g 셤 à g δ

ABP25654 standard; protein; 676 AA

RESULT 13

(first entry)

02-JUL-2002 ABP25654;

ABP25654 ID ABP2 XX AC ABP2 XX DT 02-J

10; EKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGG 115 301 LLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSE 174 LILGGFWQVFVIFGLHWGLVPVAINNLTVLGHDPILAMTFGASFAQIGAVLAVFFKSRNK 361 KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234 GFLGVVSIDAP-----DMVMFLVCAVVTFFIAFGAALAYGL-----YLVRRNGSIDPDA 283 GIFGLPNFFKPGSGISGEFWWVVIAIVISFILGFILTYVVGFKDPADVVVEQSNIVE--- 478 -----GBTLIERET-----IPAFVVGEIVTLADVKDEAFSSGALGKGVAIIPT 521 KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGD 403 2 AMVFPSL--VNGYDVAATWAAG---EMPMWSLF-GLDVAQAGYQGTVLFVLVVSWILATI 242 EKGFKKIIPDVIKTFVVPFCTLLIVVPITFIVIGPIATWAĞQLLGAĞTIWVYNLSPIIAĞ

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in such as a vaccine or diagnostic composition. The disease caused by used as a vaccine or diagnostic composition. The disease caused by streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity encoder and active acids and distinguishing/identifying
                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 LHKRLKGTADFLITPVLTLLLTGFLTFIALGP----AMRWVGDVLAHGLQGLYDFGGPVG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ---GLLFGLVYSPIVITGLHQSFPPIELBLFNQGGSF---IFATASMANIAQGAACLAVF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 FLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAMVFPSLVNGYDVAATMAAGEMPNWSL-FG-LDVAQAGYQGTVLPVLVVSWILATIEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 WLFGAIFGALYAPFVITGLHHMINALDTQLIADTKTHTTGLWFMIALSNIAQGSAVLAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.1%; Score 663.5; DB 5; 35.3%; Pred. No. 1.1e-56; iive 82; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3202-3203; 4525pp; English.
 Streptococcus polypeptide SEQ ID NO 484
                                                                                                                                                                                                                                                           27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                          29-OCT-2001; 2001WO-GB004789
                                                                                                                Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                        (GENO-) INST GENOMIC RES
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABN66285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 676 AA;
                                                                                                                                                   WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                           Telford J, I
Tettelin H;
                                                                                                                                                                                      02-MAY-2002.
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Exteriorous teracus to an instruction deliberative incomposition one of 10 fully defined sequences given in the (or comprishing 40 one of 10 fully defined sequences given in the (or comprishing 40 one of 10 fully defined sequences given in the (or comprishing 40 one of 10 fully defined sequences given in the incleid acids, its complement or sequences hybridishing to it). Also included are a crecombinant vector comprishing the mucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the mucleic acid. The nucleic acids are consen from 3654 disclosed sequences encoding 3654 disclosed proteins. Or the nucleic acids is useful for diagnosing pathological conditions resulting from E. faccium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the mucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents one if the disclosed E. faecium proteins.
                                                                     343
                                                                                                                                           403
                                                                                                                                                                            617
                                                                                                 ---VIASTTETKSAKEKAVVSGTKLSVVSPLSGLAKPLDQASDPVFSQGIMGKGVVIDPS 561
                                                                                                                                                                                                           EVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGL-GEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                   New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial infection.
AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAY---GLYLVRRNGSIDPDAT
                       285 AAPVPAGTTKAE-AEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                                                                        562 DGELVSPVDATVSVLFFTXHAIGLLT----SEGVEFLIHIGMDTVNLEGKGFTSHVAQGD
                                                                                                                                           KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine, urinary tract infection, bacteraemia, endocarditis, wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 5288; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              E. faecium protein sequence SEQ ID 5288,
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                                                                                                                                                                                                                                                                                                                                         ADC95661 standard; protein; 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00107532
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADC92007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                            ADC95661;
                                                                                                                                                  344
                                                                                                                                                                                                                                                     618
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575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLLFGLVYSPIVITGLHQSFPPIE-LELFNQGGSFIFATASMANIAQGAACLAVFFLAKS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP 287
                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                59 LHKRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGL----YDFGGPVG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 VPAGITKABABABABRSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPIKGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr GJ;
                                                                                                                                                                                                       293 GLIMGSLWOVFVMFGNHWGFVPIMFLNIEQYGFDVIMPMLLPAILAQGGAALAVALRTKD
                                                                                                                                                                        1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDV - - AQAGYQGTVLFVLVVSWILATIEKF
                                                                                                                     56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                   Length 628
                                                                                                                        Indels
                                                                28.0%; Score 662; DB 7; L. 33.5%; Pred. No. 1.4e-56; ive 89; Mismatches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|| |||:||:||:||:|
GDLLIRFDIBAIRAAGYSVITPVVITN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU37874 standard; protein; 627 AA.
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23-MAY-2000; 2000US-0206648P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578F.
27-NOV-2000; 2000US-0253625F.
22-DEC-2000; 2000US-0257331P.
16-FEB-2001; 2001US-0269331P.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae.
                                                                                                                                 160; Conservative
                                                                           Query Match
Best Local Similarity
                         Sequence 628 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU37874;
                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes there later the prokaryotes used are Escherichia configuration of proteins. The prokaryotes used are Escherichia selected in Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Seudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous of organisms. The present sequence represents an essential prokaryotic cludar proliferation protein. Note: The sequence data for this patent of calcular proliferation protein. Note: The sequence data for this patent of electronic form part of the printed specification, but was obtained in the way of the proposition of programme for the printed sequences. New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids. Example 3; SEQ ID NO 13467; 511pp; English. WPI; 2001-611495/70 N-PSDB; AAS55733

Sequence 627 AA;

26; Gaps Length 627; 27.9%; Score 660; DB 4; Length 62' 34.3%; Pred. No. 2.1e-56; ive 92; Mismatches 187; Indels Query Match
Best Local Similarity 34.39
Matches 159; Conservative

61 KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120 9 1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH g G à à g

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AFPSGHAFAVRIKAEDGSNVDIIMHIGFPTVNINGTHFNPLKKQGDBVKAGELLCEFDID 417 358

AIKAAGYEVITPIVVSN---YKKIGPVNTYGLGEIEAGANLLNV 458

418

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